

Best Local Similarity 84.2%; Pred. No. 4.3e-66;
Matches 529; Conservative 0; Mismatches 94; Indels 5; Gaps 3;

```

QY 164 aagattgattgaggaagtgcttctcattgattgagtgctgattcctctatacc 223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28 AAGTTTAAATCTCGGAGAAATGGCTTCTGCTTGGCTATCGGATGCTTATACCT 87
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 224 tctgtgttcacagcagcttggtct---ctatgcttccaaatgctgagataaaagttaac 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88 TTCTGATAAGCACACATTTGGCTGTACTTCATCTTCAGACACCGAGATAAAGTTAAC 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 281 ctctccagatttgagatagtgagccctggatattttaggttatctctcttgcgaatg 340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 148 CTCCTCAGCA-TTTCAGATAGTGGATCCGGATACCTAGTATCTCTATTTCGAATGGC 206
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 341 aacctccattttccggataattttaaggaatcaccaatagaatgaataataacc 400.
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 AACCCCACTGCTCTGTCGATCATTTTAAAGATGCGACATGGAATATGAATATAATACC 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 401 gaaacattgatagtgaaactggagaccattaccacaaagaatctacattacaaagatg 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 GAAACATTTGGTAGTGAACATGGAAGACCATCATTTACTTAAGATCTACATTACAAGATG 326
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 461 ggtttgattctaaagaaggtattgaagcaagaataaacacacactctctgcagcacaatgca 520
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 327 GGTGTTGATCTTAACAGGGCATTGAAGCGAAGATACACACGCTTTTACCATGGCAATGCA 386
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 521 caaatgattcagaaagtttagaagttcattggcagaaactactatttgacatcacacaag 580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 387 CAATGATGATGAGATGTTCAAGTTCCTGGCGAAGAACTACTTATTGGATATCACCAAG 446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 581 gaaatcgggaaactaaattcaagatggactgtgtattatacaactggcaattattag 640
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 447 GAATTCAGAAACTAAAGTTTCAAGATATGATGCGTATATTACAAATGGCAATATTATAC 506
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 641 tctgctctgaaactggcattgggtgctcattttgtacaaattaccagttg-ttttac 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 507 TCTGTTCTTGGAACTGGCATAGGTGTACTTCTTGATACCAATTACAACTGTTTTTAC 566
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 700 tggatgagggcttgaccattcagcagagtgactgattacattacaaagggttaaggaaaa 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 567 TGCTATGAGGCTTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 626
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 760 aatatggatgaggtttccctatttgg 787
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 627 AATATAGGATGCAGATTTTCCCTATTG 654
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 6
AI798934/c

LOCUS AI798934 676 bp mRNA linear EST 18-DEC-1999
DEFINITION we94e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2348766 3', similar to SW:1132_HUMAN Q14627 INTERLEUKIN-13
RECEPTOR ALPHA-2 CHAIN PRECURSOR ; mRNA sequence.

ACCESSION AI798934
VERSION AI798934.1 GI:5364406
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 676)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert Length: 882 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 468.

JOURNAL COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert Length: 882 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 468.

FEATURES

Source
1..676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2348766"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-CGAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 205 a 133 c 117 g 221 t
ORIGIN

Query Match 26.7%; Score 387.8; DB 9; Length 676;
Best Local Similarity 76.5%; Pred. No. 1.7e-57;
Matches 518; Conservative 0; Mismatches 147; Indels 12; Gaps 3;

```

QY 754 ggaataaatggtgagcaggttccctatttggagtcacagactataaagattctac 813
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 676 GGACACAAATAGGATGCAGATTTCCCTATTTGGAGCATCAGACTATAGAGATATCTAT 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 814 atctgttgaatgggtcagatccagatccagcctatcagaccagctattttttttcag 873
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 616 ATTTGCTAATGGATCATCAGAGACGAGCCTATCATGATCCAGTATTATTCACCTGTCAG 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 874 ctcaataatagtttaaacctatgccaccagactccttagtcttacttgagagaattca 933
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 556 CTTCAAAATATAGTTAAACCTTTGCCCCAGTCTATCTTACTTTTACTCGGAGAGTTCA 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 934 gaggaaattaactgaaatggaactgcctaaaggagccattccagcgaattgttcatt 993
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 TGTGAATTAAGCTGAAATGGAGCATACCTTTGGGACCTATTCCAGCAAGGTGTTTGAT 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 994 tatgaattgaattcagagagtggtactacttgggtgactaccagcttgagagatgag 1053
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 436 TATGAATTTGAGATCAGAGAAGATGATACCCACTTGGTACTGCTACAGTTGAAATGAA 377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1054 atacaaatcacagaacatcaaatgaaagccaaataattgcttttggtaagaagtaaa 1113
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 ACATACACCTTGAAACACAAATGAACCCGACAATTATGCTTTGTAGTAAGAGCAAA 317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1114 gtaataattattgctcagatgatggaatctggagtgagtgagtgatgaacaatctgg 1173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 316 GTGAATATTATTGCTCAGATGGCGAATTTGGAGTGAGTGAGTGATAAACAATGCTGG 257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1174 aaagtg---acatatggaaggaaaccccttagtattttttgtgataccatttgcctttgtc 1230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 256 GAAGTGAACCTATCGAAGAAAACTTTGTACGCTTTCTGGCTACCAATTGTTGTTTCATC 197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1231 tcaataattgtttgtgtaataactgctgtcttttggtaagaagaaggtcttaactgaaa 1290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 196 TTAATATTAGTTATATTGTAACCGCTGTGCTTTTGGCTTAAGCCAAACCCCTACCCAAA 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1291 acgat-----cttcatacaaaaaaagaagctctttctcatcaagacacattctgtg 1343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 136 ATGATTCAGAAATTTTCTGTGATACATGAAGACTTCCATATCAAGAGACATGATATG 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1344 actcagtaacttcagctcttattgcccagatgttaaatatgagctcttataaagaaact 1403
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 76 ACTCAACAGTTTTCAGATC--ATGGCCAAATGTTCAATATGAGTCTCAATAAATGAATTT 19
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1404 tttcctcaaatattgaa 1420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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/dev_stage="7 months"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

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BASE COUNT      186 a  119 c  146 g  198 t
ORIGIN

Query Match      18.7%; Score 271.2; DB 10; Length 649;
Best Local Similarity 72.9%; Pred. No. 2.2e-37;
Matches 411; Conservative 0; Mismatches 133; Indels 20; Gaps 4;

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```

Qy 39 gaagggaagtcagagattcctaataatgtctcacaactggagagagaaaaaagag 98
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GAAGGAAACAGTAGAGATTCAATTTAGTGCT-----AATGGGAAGAGGACAAAGAG 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 99 gacctgtgataattgcctatgataattcattcttgagaaccattattgagtgga 158
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 57 GTCITGTGTAACCTGCTGATATACATTTCTTGAGAACCATATTTATGAGTAGAGC 116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 159 cttcaagaattgaatcttgagggaatgcttctcattcatttggtgcgattcctcta 218
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 117 TTTGAGCACACTAATCTCGGAAATGGCTTT-----TGTCATATCAGATGCTTGTG 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 219 taccctgtcttgacagacattggtgctctatgcttccaaatgctgagataaaagttaa 278
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 171 TTTCAATCTCTTTGTACAAATAACTGGCTAT-----TCTTTGGAGATAAAAGTTAA 221
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 279 tctctcaggatttgtagatagtgaccctggatattagttatctctctcttgcgaatg 338
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 222 TCCCTCTCAGGATTTGAAATATTTGGATCTCGGATTAATTTGTTATCTATTTGCAATG 281
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 339 gcaacctccattatttccgggataatttaaggaatgcacaaatagaatgaattaaaata 398
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 282 GAAACCTCTCTGGTTATAGAAAATTTAAGGGCTGTACACTAGATAATAGTAAATA 341
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 399 ccgaaacattatagtagtaaaactggaagaccatcattaccagaatctacattacaaga 458
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 342 CCGAAATTTTGTACGCGACAGCTGGAAGACTATAATTAAGGAATCAATTTTCAAGGA 401
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 459 tgggttgatcttaacaaagtattgaagcaagaataaacacactctgcccagacacatg 518
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 402 TGGTTTGATCTTAATAAGGCATTTGAAGGAAGATACGTAAGCAATTTGTGAGACCATG 461
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 519 cacaataggga-tcagaagttagaagttcattgggagaaactacttattggacatcacac 577
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 462 TACCACGTGACTCAGAGTACCAAGTCCATGATCGAGAGCTCTTATGGGACTCTCCGAT 521
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 578 aagggaatcgggaaactaaaattc 601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 522 GAAGGAGTTTGGAAACTCAATTC 545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 14
AA298563
LOCUS      EST114178 HSC172 cells I Homo sapiens cDNA 5' end similar to IL13
DEFINITION receptor (IL13R), mRNA sequence.
ACCESSION AA298563
VERSION   AA298563.1 GI:1950896
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 365)
AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
           ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
           ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

```

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.T., Pelligrino,S.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudik,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

96026280
Other_ESTs: THCI94124
Contact: Kerlavage, AR

Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
source
1..365
/organism="Homo sapiens"
/db_xref="ATCC (Inhost):178283"
/db_xref="taxon:9606"
/clone_lib="HSC172 cells I"
/cell_type="fibroblast"
/cell_line="HSC172 (16PDL)"
/dev_stage="fetal"
/note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
; Site_2: XhoI"

BASE COUNT 106 a 66 c 69 g 123 t 1 others
ORIGIN

Query Match 18.2%; Score 264.4; DB 9; Length 365;
Best Local Similarity 86.3%; Pred. No. 4e-36;
Matches 303; Conservative 0; Mismatches 47; Indels 1; Gaps 1;

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Qy 563 attggacatcaccaaggaatcggaactaaattcaagatatgactgtgtatatt 622
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATTTGATATCACCAAGGAATTCAGAAACTAAAGTTTCAGATATGATGCGTATTATT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 623 acaactggcaatatttagtctgtctcttggaaacctggcattggcatttccatttgatacca 682
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ACAATTGGCAATATTACTCTGTTCTTGGAAACCTGGCATAGGTGCTACTTCTTGATACCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 683 attaccagttgttttactggtatgagggcttggaccattcagcagagtgactgattaca 742
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ATTAACAATCTTTTACTGGTATGAGGGCTTGGTTTCATGTCATACAGTGTGTGATTACA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 743 tcaaggttaatggaaaaaatatggatcaggtttccctatttggagtcacagactata 802
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 TCAAGGCTGATGGACAAATATAGATGATGATTTCCCTATTGAGGCATCAGACTATA 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 803 aagattttacatctgtgttaatgggtcatcagaatccagctccatccagccagctatt 862
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 AAGATTTCTATATTGTGTTAATGATCATCAGAGANCAAGCTCATCAGATCCAGTTATT 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 863 tta-tttttcaggttcaaaatagtttaaacctatgcccacagactacctt 912
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TCACCTTTCCAGCTTCAAAATATAGTTAAAGCTTTTGGCGCGAGCTCTATCCT 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 10:52:12 : Search time 4150.53 Seconds
(without alignments)
2016.155 Million cell updates/sec

Title: US-09-828-995B-54
Perfect score: 620
Sequence: 1 ggcacgagctgagttgtg.....caagatatgactgtgtata 620

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_estl:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	341.2	55.0	954	9	AL525497
2	336.6	54.3	683	10	BG778615
3	328.2	52.9	743	10	BG723203
4	323.2	52.1	658	10	B1828427
5	271.2	43.7	649	10	BE289033
6	261.4	42.2	476	10	BF443846
7	248	40.0	379	10	BF443844
8	192.4	31.0	473	10	R52795
9	188.6	30.4	928	9	AL562513
10	188.2	30.4	904	10	B1462644
11	142.4	23.0	715	10	BE788633
12	116.6	18.8	755	10	BE619361
13	49.6	8.0	942	12	CNS018GS
14	45.4	7.3	1101	12	CNS0039G
15	45.2	7.3	365	9	AA298563
16	45.2	7.3	840	12	BH153955
17	44.6	7.2	1101	12	CNS0039G

C 18	44	7.1	1001	12	CNS0064G
C 19	43.2	7.0	791	12	AQ865293
C 20	43	6.9	641	12	AZ523481
C 21	43	6.9	645	12	AZ522162
C 22	42.8	6.9	704	10	BM163666
C 23	42.8	6.9	879	12	AZ678808
C 24	42.6	6.9	579	12	CNS00F20
C 25	42.6	6.9	639	12	CNS017QD
C 26	42.6	6.9	903	12	CNS00IIC
C 27	42.4	6.8	481	9	AW305472
C 28	42.4	6.8	513	9	AL516344
C 29	42.4	6.8	549	12	CNS0248Y
C 30	42.4	6.8	677	12	B89641
C 31	42.4	6.8	1013	9	AL564621
C 32	42.2	6.8	928	10	BF274633
C 33	42.2	6.8	1025	12	CNS014J2
C 34	42	6.8	984	12	CNS01POS
C 35	41.8	6.7	438	12	AQ132259
C 36	41.8	6.7	928	12	CNS06DH6
C 37	41.4	6.7	1223	12	B12981
C 38	41.2	6.6	982	12	CNS006BE
C 39	41	6.6	461	12	B67180
C 40	41	6.6	908	12	BH138952
C 41	40.8	6.6	390	12	AQ125679
C 42	40.8	6.6	1101	12	CNS000NX
C 43	40.6	6.5	812	12	CNS00IDC
C 44	40.6	6.5	928	12	CNS00DKY
C 45	40.6	6.5	998	12	AZ680790

ALIGNMENTS

RESULT 1
AL525497
LOCUS
DEFINITION AL525497 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC012YF21 5 prime, mRNA sequence.
ACCESSION AL525497
VERSION AL525497.1 GI:12788990
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES source

1. .954
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC012YF21"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 295 a 172 c 201 g 285 t 1 others

VERSION BI28427.1 GI:15939977
KEYWORDS
EST. human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 658)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL

```

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1423 row: i column: 21
High quality sequence stop: 651.
Location/Qualifiers
1. .658
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5170268"
/clone_lib="NIH_MGC_llg"
/tissue_type="medulla"

FEATURES
source

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/Note="organ: brain; vector: pUMV-SPOKRB; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note
this is a NIH_MGC Library."
BASE COUNT      202 a  121 c   141 g   194 t
ORIGIN

Query Match      52.1%; Score 323.2; DB 10; Length 658;
Best Local Similarity 84.3%; Pred. No. 1.9e-63;
Matches 388; Conservative 0; Mismatches 68; Indels 4; Gaps

```

[illegible]


```

Qy 151 agtggaaactcaagattgaattcttgaggagaatggcttctcattcatttgatgcgga 210
|||||
Db 150 AGTGGAAACTTCAAGGTATTAATCTTAGAGAAATGGCTTTATTTCATGTGAATATCAGA 209
|||||
Qy 211 ttcctctataccctgctgttggtagacagcatttggctcta---tgctttcaaatgctgag 267
|||||
Db 210 TGTCTATATACCTCTCTTATTGTCACAGCATTTGGCTCTACTTTGCTCTCAAAATGCCGAG 269
|||||
Qy 268 ataaaagttaactctcctcaggattttgagatagtggaacctggatatttaggttatctc 327
|||||
Db 270 ATAAAGTTAATCTCTCCACAGATTTGAATAATAGTGGACCTCGATATTTAGGTTATCTC 329
|||||
Qy 328 tcttggcaatggcaacctccattatttccgggataattttaagggaatgcacaaatgagat 387
|||||
Db 330 TATTTGGAGTGGCAACCTCCACTGCTCTCGATAATTTAAAGGAATGCACAGTAGAGTAT 389
|||||
Qy 388 gadttaaatgcgaadattgagtaggaadactgggaagaccattacdaagaatcta 447
|||||
Db 390 GAATTAATAATACCGAAACATTGATAGTGAAGCTGGAAGACGATCATTTACTTAAGAATCTA 449
|||||
Qy 448 catlaccdaagatgggtttgatcttaac 474
|||||
Db 450 CATTACAAAGATGGGTTTGATCTTAAC 476
|||||

RESULT 7
LOCUS BF443844 379 bp mRNA linear EST 01-DEC-2000
DEFINITION 261483 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BF443844
VERSION BF443844.1 GI:11503936
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 379)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCGATCAGCAGC
Plate: 95 row: 0 column: 4
Seq primer: ATTTAGCTGACACTATAG.
FEATURES
source
Location/Qualifiers
1. .379
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 124 a 61 c 69 g 125 t
ORIGIN

Query Match 40.0%; Score 248; DB 10; Length 379;

```

```

Best Local Similarity 89.5%; Pred. No. 2.2e-46;
Matches 290; Conservative 0; Mismatches 30; Indels 4; Gaps 2;

Qy 154 ggaactccaagtattgaattcttgaggagaatggcttctcattcatttgatgcgattc 213
|||||
Db 57 GGAACCTTCAAGGTATTAATCTTAGA-GAATGGCTTTATTTCATGTGAATATCAGATGT 115
|||||
Qy 214 ctctataccctgctgttggtagacagcatttggctcta---tgctttcaaatgctgagata 270
|||||
Db 116 CTATATACTCTCTCTTATTGTCACAGCATTTGGCTCTACTTTGCTCTCAAAATGCCGAGATA 175
|||||
Qy 271 aaagttaactctcctcaggattttgagatagtggaacctggatatttaggttatctctc 330
|||||
Db 176 AAAGTTAATCTCTCCACAGATTTGAAATAGTGGACCTCGATATTTAGGTTATCTCTAT 235
|||||
Qy 331 ttgcaatggcaacctccattatttccgggataattttaagggaatgcacaaatgagata 390
|||||
Db 236 TTGAGTGGCAACCTCCACTGCTCTCGATAATTTAAAGGAATGCACAGTAGATATGAA 295
|||||
Qy 391 ttaataaccgaaacattgatagtgaaacctgggaagaccattaccagaatctacat 450
|||||
Db 296 TTAATAATACCGAAACATTGATAGTGAAGCTGGAAGACGATCATTTACTTAAGAATCTACAT 355
|||||
Qy 451 taaaaagatgggtttgatcttaac 474
|||||
Db 356 TACAAAGATGGGTTTGATCTTAAC 379
|||||

RESULT 8
LOCUS R52795 473 bp mRNA linear EST 18-MAY-1995
DEFINITION y999f10.r1 Soares infant brain IN1B Homo sapiens cDNA clone
IMAGE:41648 5', mRNA sequence.
ACCESSION R52795
VERSION R52795.1 GI:814697
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 473)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasakis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1454
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1454 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 372.
Location/Qualifiers
1. .473
/organism="Homo sapiens"
/db_xref="GDB:414189"
/db_xref="taxon:9606"
/clone="IMAGE:41648"
/clone_lib="Soares infant brain IN1B"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
FEATURES
source
Location/Qualifiers

```


for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 210 a 375 c 145 g 174 t
ORIGIN

Query Match 30.4%; Score 188.2; DB 10; Length 904;
Best Local Similarity 77.9%; Pred. No. 9.4e-33;
Matches 306; Conservative 0; Mismatches 73; Indels 14; Gaps 6;

Qy 150 gagtggaaactcaaaagttaaatctgtggaggaatgagccttcatttcatttgatgtcg 209
Db 27 GAGAGGCAATATCAAGGTTTAAATCTCGGAGAAATGGCTTTCGTTGGCTATCGG 86

Qy 210 attcctctatccctgctgtttcacagcatttgctc---ctatgctttcaaatgcgga 266
Db 87 ATGCTTATATACCTTCCTGTAAGCAACCAATTTGGCTGTACTTTCATCTTCAGACCCGA 146

Qy 267 gataaaagttaatcctcctcaggttttgagatagtggaacctggtatattaggttatct 326
Db 147 GATAAAAGCTTAACCTCTCCTCAGGATTTTGAGATAGTGATCCCGGATACTTATAGGTTATCT 206

Qy 327 ctctttgcaatggaaacctccattatttcogataa---tttaagaagaatgcacaatag-- 382
Db 207 CTATTTGCAATGGCAACCCCACTGTCTCTGGATCATCTTTAAACGGAAATGCACAGTGCA 266

Qy 383 aatatgaattaaataccgaacatttgata---gtgaaacctggaagaccattcattacca 439
Db 267 CATATGAACCTAAATACCGAACAATTTGTAGTGTAACACATGCGCAAGACCATCATCTACTA 326

Qy 440 agaattcattacaaagtgggttgatcttaacaaagg---tattgaagcaaatgataa 496
Db 327 AGAATCTACATTACAAAGATGGTTTGATCTTAACAAAGGCACCTCTGAACGCGAAGATAC 386

Qy 497 acac-actctcgcagcaaatgcacaatgga 528
Db 387 ACAGCGCTTTTACCATGGCAATGCAAAATGGA 419

RESULT 11
BE788633
LOCUS 601475992F1 NIH_MGC_68 715 bp mRNA linear EST 20-OCT-2000
DEFINITION 601475992F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878831 5',
mRNA sequence.
BE788633
VERSION BE788633.1 GI:10209831
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 715)
NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/BTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9643 row: g column: 24
High quality sequence stop: 575.
Location/Qualifiers
1. 715
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3878831"

FEATURES
source

/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SpORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life Technologies."

BASE COUNT 229 a 154 c 141 g 191 t
ORIGIN

Query Match 23.0%; Score 142.4; DB 10; Length 715;
Best Local Similarity 81.6%; Pred. No. 2.4e-22;
Matches 191; Conservative 0; Mismatches 36; Indels 7; Gaps 2;

Qy 394 aaataccgaacatgatgtgaaacctggaagaccattcattaccaagaatcattac 453
Db 5 AAATACCCGAACATTTGGTAGTGAACATGGGAAGACCATCATTTACTAGAAATCTAGATTAC 64

Qy 454 aaagatgggttgatcttaacaaaggattgaagcaaaagataaaacacactcttgc---a 510
Db 65 AAAGATGGGTTTGATCTTTAAACAAGGCGATTGAAGCGAAGATACACACGCTTTTACCTAT 124

Qy 511 gcacaatgcacaaatggatca---gaagttagaagttcatagggcagaaactactattg 566
Db 125 GCGCAATGGCAAAACTGGCATACGCAAGTTCAAAGTTCTCTGGCAGAACTACTTATTG 184

Qy 567 gacatccacacaaagaaatcgggaacataaaattcaagatatggactgtgata 620
Db 185 GATATCACCAACGAAGAAATCCAGAAACTAAAGTTCCAGGATATGGATTGGTATA 238

RESULT 12
BE619361
LOCUS 601473366F1 NIH_MGC_68 755 bp mRNA linear EST 20-OCT-2000
DEFINITION 601473366F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876064 5',
mRNA sequence.
BE619361
VERSION BE619361.1 GI:9890299
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 755)
NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/BTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9636 row: d column: 17
High quality sequence stop: 685.
Location/Qualifiers
1. 755
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3876064"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SpORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life Technologies."

BASE COUNT 228 a 131 c 177 g 219 t
ORIGIN

Query Match		18.8%;	Score 116.6;	DB 10;	Length 755;
Best Local Similarity		74.0%;	Pred. NO. 1.8e-16;		
Matches 270;		Conservative 0;	Mismatches 79;	Indels 16;	Gaps 9;
QY	161	tcaaaatttgatcttgcgaggaatggcttcattcatttggatgctgattccctctata 220			
Db	3	TCAAGGTTTAAATCTCGGAGAAAGGGCTTCGTT-GCTTGGTAATCGGATGCTTATATA 61			
QY	221	ccctgcttgtttgcacagcatt---tggctctatgctttcctaagtctgagataaaagtta 277			
Db	62	CCTTCTTGATAGACACAACATTTGGCTGTACTTCATCTTACAGACACCGAGATAAAGGTA 121			
QY	278	atcctcctcaggaatttggagatg-tgaacctcgatatttaggttatct--ctctttgc 334			
Db	122	ACCTCTCTCAGGATTTTGAGATAGTAGGATCCGGATACCTTAGGTATCTCGGTATTTCG 181			
QY	335	aatggcaacctccattatttcc---ggataattttaaggatgc--acaatagaatatg 388			
Db	182	AATGCCAACCCGGCCACTGCTCTCGGATCAGTTTAAAGGAATGCTAGCAGTGGAAATG 241			
QY	389	aa-ttaaataccgaaacattgatgtaaaactggaagaccatc-attaccaagaatct 446			
Db	242	AACATAAAATACCGAAACATGCTAGTGAACATCTGGAAGACCATCTATTACTAAGAATCT 301			
QY	447	acattac-aagatgggtttgatcttaacaaaggattgaagcaagaataaacacacttc 505			
Db	302	AGATTACGGAAGATGGTTGGATCTTAACAGGGCATAGAGCGAAGATACACACGCTTT 361			
QY	506	tgcca 510			
Db	362	GACCA 366			
RESULT 13					
CNS018GS/c					
LOCUS					
DEFINITION					
Drosophila melanogaster genome survey sequence T7 end of BAC					
BACN13P09 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.					
ACCESSION					
AL109318					
VERSION					
AL109318.1 GI:5629622					
KEYWORDS					
GSS.					
SOURCE					
fruit fly.					
ORGANISM					
Drosophila melanogaster					
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)					
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.					
FEATURES					
source					
1..942					
/organism="Drosophila melanogaster"					
/plasmid="pBelOBAC11"					
/db_xref="taxon:7227"					
/clone_lib="DrosBAC"					
/clone="BACN13P09"					
/note="end : T7"					
BASE COUNT					
ORIGIN					
155 a 77 c 70 g 494 t 146 others					

Query Match		8.0%;	Score 49.6;	DB 12;	Length 942;
Best Local Similarity		37.2%;	Pred. NO. 0.31;		
Matches 73;		Conservative 42;	Mismatches 81;	Indels 0;	Gaps 0;
QY	348	attatttccggataattttaaggaaatgcacaaatataataataataaccgaaacat 407			
Db	302	AWWATWACCWAAMAAWMAAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAA 243			
QY	408	tgatagtgaacacggaagaccatcattaccagaatcttaccacaagatggtgttga 467			
Db	242	AAWAAWAAWAAWTTTAWTAAWAAWAAWTTGAWAAWAAWTTMGTTTAAWAAATCGTTANGA 183			
QY	468	tcttaacaaggattgaagcaagaataaacacactcttccagcacaaatgcacaaatgg 527			
Db	182	AAWAAWAAWAAWMAWMAAAATAWAAWAAWMAWMAWMAWMAWMAWMAWMAWMAWMAW 123			
QY	528	atcagaagttagaagt 543			
Db	122	WMAWAAWMAWMAAAAGT 107			
RESULT 14					
CNS0039G					
LOCUS					
DEFINITION					
Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.					
ACCESSION					
AL063921					
VERSION					
AL063921.1 GI:4941778					
KEYWORDS					
GSS.					
SOURCE					
fruit fly.					
ORGANISM					
Drosophila melanogaster					
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)					
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.					
FEATURES					
Location/Qualifiers					
1..1101					
/organism="Drosophila melanogaster"					
/db_xref="taxon:7227"					
/clone_lib="RPCI-98"					
/clone="BACR08K10"					
/note="end : TET3"					
BASE COUNT					
ORIGIN					
201 a 64 c 131 g 202 t 503 others					

Query Match		7.3%;	Score 45.4;	DB 12;	Length 1101;
Best Local Similarity		19.3%;	Pred. NO. 2.8;		
Matches 98;		Conservative 184;	Mismatches 227;	Indels 0;	Gaps 0;

Bioinformatics
The Institute for Genomic Research
7112 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgl/hgl.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
1. .365
/organism="Homo sapiens"
/db_xref="ATCC (inhost):178283"
/db_xref="taxon:9606"
/clone_lib="HSCI72 cells I"
/cell_type="fibroblast"
/cell_line="HSCI72 (16PDL)"
/dev_stage="fetal"
/note="Organ: lung; Vector: pBluescript SK-; Site_1: ECORI
; Site_2: XhoI"
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BASE COUNT
ORIGIN

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Best Local Similarity 86.3%; Pred. No. 2.8;
Matches 50; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 563 attggacatcacacacagggaattcgggaactaaaactcaagatataggactgtgtata 620
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Db 1 ATTTGGATATCACCACAAAGGAATTCAGAAACTAAAGTTCAGGATATGGATGCGGTATA 58

Search completed: September 23, 2002, 13:33:52
Job time: 9700 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 11:31:42 ; Search time 108.29 Seconds
(without alignments)
1406.342 Million cell updates/sec

Title: US-09-828-995B-54
Perfect score: 620
Sequence: 1 ggcacgagctgagttgtg.....caagatatggactgtgtata 620

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	341.2	55.0	1369	1	US-08-609-572-3
2	341.2	55.0	1369	4	US-08-841-751-3
3	341.2	55.0	1369	4	US-08-846-340-3
4	341.2	55.0	1369	4	US-08-846-344-3
5	311.2	50.2	1525	1	US-08-609-572-1
6	311.2	50.2	1525	4	US-08-841-751-1
7	311.2	50.2	1525	4	US-08-846-340-1
8	311.2	50.2	1525	4	US-08-846-344-1
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11	35.2	5.7	4797	4	US-09-354-243B-25
12	35.2	5.7	5836	4	US-09-233-086-2
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14	34.4	5.5	1956	4	US-08-559-896B-1
15	33.8	5.5	1991	4	US-08-235-836C-69
16	33.8	5.5	1991	4	US-08-235-836C-77
c 17	33.8	5.5	43795	3	US-08-742-185-101
c 18	33.6	5.4	3058	4	US-09-276-531-107
19	33.4	5.4	9636	1	US-08-323-170B-1
20	33.4	5.4	9636	4	US-08-954-441-1
c 21	33	5.3	2081	4	US-08-235-836C-67
c 22	33	5.3	3350	3	US-08-617-860B-3
c 23	32.8	5.3	1789	1	US-08-393-219-1
c 24	32.8	5.3	5322	3	US-09-058-489-13
c 25	32.6	5.3	2831	1	US-08-453-695A-108
c 26	32.6	5.3	2831	1	US-08-268-161A-108
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c 29	32.6	5.3	2831	5	PCT-US95-08071-108	Sequence 108, App
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c 31	32.4	5.2	8700	2	US-08-466-961A-16	Sequence 16, Appl
c 32	32.4	5.2	8700	2	US-08-645-193B-18	Sequence 18, Appl
c 33	32.4	5.2	43795	3	US-08-742-185-101	Sequence 101, App
c 34	32.2	5.2	2493	3	US-08-945-056-3	Sequence 3, Appl
c 35	32.2	5.2	3827	1	US-08-170-294-6	Sequence 6, Appl
c 36	32.2	5.2	3827	2	US-08-664-855-6	Sequence 6, Appl
c 37	32.2	5.2	3827	2	US-08-718-751-1	Sequence 1, Appl
c 38	32.2	5.2	3827	3	US-09-049-289-6	Sequence 6, Appl
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c 40	32	5.2	2615	1	US-08-759-446-1	Sequence 1, Appl
c 41	32	5.2	2615	4	US-09-027-998A-1	Sequence 1, Appl
c 42	32	5.2	3050	2	US-09-031-442A-21	Sequence 21, Appl
c 43	32	5.2	3050	4	US-09-258-377-21	Sequence 21, Appl
c 44	31.8	5.1	2356	1	US-08-105-483-222	Sequence 22, App
c 45	31.8	5.1	2356	1	US-08-220-151-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-08-609-572-3
; Sequence 3, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whittiers, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
US-08-609-572-3

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Query Match 55.0%; Score 341.2; DB 1; Length 1369;
Best Local Similarity 84.0%; Pred. No. 2.6e-85;
Matches 398; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

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RESULT 2
US-08-841-751-3
; Sequence 3, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A. 32,724
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: G15268
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TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
US-08-841-751-3

Query Match 55.0%; Score 341.2; DB 4; Length 1369;
Best Local Similarity 84.0%; Pred. No. 2.6e-85;
Matches 398; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

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US-08-846-340-3
; Sequence 3, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
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RESULT 5
US-08-609-572-1
; Sequence 1, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
US-08-609-572-1

Query Match 50.2%; Score 311.2; DB 1; Length 1525;
Best Local Similarity 74.8%; Pred. No. 5.3e-77;
Matches 437; Conservative 0; Mismatches 128; Indels 19; Gaps 3;
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Qy 277 aatcctctcaggatttggatagtagtgacctggatatttaggttatctctctcttgcacaa 336
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Db 634 GAAGGAAGTTGGAAACTAAAATTCAGGACATGAAGTGTATATA 677

RESULT 6
US-08-841-751-1
; Sequence 1, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
US-08-841-751-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1525 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1404
US-08-841-751-1

Query Match 50.2%; Score 311.2; DB 4; Length 1525;
Best Local Similarity 74.8%; Pred. No. 5.3e-77;
Matches 437; Conservative 0; Mismatches 128; Indels 19; Gaps 3;
Qy 37 aggaaggagcttagagattcctaataatgctctccaaactggagagagagagagagagagag 96
Db 113 AGGAAGGAAACAGTAGAGATTCAATTTAGTGTCT- - - - -AATGTGGAAGGAGGACAAAG 168
Qy 97 aggaacctgataattgacctatgataattcattcttggagaaaccattattttagtgga 156
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Qy 337 tggcaacctcattatttcccggaataatttgaaggagatgcacataatagaatgaattaaa 396
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RESULT 7
US-08-846-340-1
Sequence 1, Application US/08846340
Patent No. 6248714
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitzer, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive

TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,340
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1525 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1404
US-08-846-340-1

Query Match 50.2%; Score 311.2; DB 4; Length 1525;
Best Local Similarity 74.8%; Pred. No. 5.3e-77;
Matches 437; Conservative 0; Mismatches 128; Indels 19; Gaps 3;
Qy 37 aggaaggagcttagagattcctaataatgctctccaaactggagagagagagagagagagag 96
Db 113 AGGAAGGAAACAGTAGAGATTCAATTTAGTGTCT- - - - -AATGTGGAAGGAGGACAAAG 168
Qy 97 aggaacctgataattgacctatgataattcattcttggagaaaccattattttagtgga 156
Db 169 AGGCTCTGTGATACTGCTGTGATAATACATTTCTTGAGAAACCATTATTATTGAGTAGA 228
Qy 157 aacttcaagattgaactctggaggagatgcttcttcattcatttggatgctgagttcctc 216
Db 229 GCTTTTCAGCACACTAAATCTCGGAGAAATGGCTTT- - - - -TGTGCATATCAGATGCTTG 282
Qy 217 tataccctgctgtttgcacagcatttgcctctatgcttccaaatgctgagataaaagt 276
Db 283 TGTTCATCTCTTTGTACAACTACTGCTAT- - - - -TCTTTGGAGATAAAGTT 333
Qy 277 aatcctcctcaggattttagagataggaccctggatatttaggttatctctcttgcag 336
Db 334 AATCCTCCTCAGGATTTTGAATAATTGGATCTGGATTTACTTGGTTATCTCTATTGTCAG 393
Qy 337 tggcaacctcattatttcccggaataatttgaaggagatgcacataatagaatgaattaaa 396
Db 394 TGGAAACCTCCTGTGGTTATGAGAAATTTAAGGGCTGTACACTAGATAATGAGTTAAAA 453
Qy 397 taccgaaacattgatgagaaactggagaccattcattacaaagaatctcattacataaa 456
Db 454 TACCGAAATGTTGATAGCGACAGCTGGAAGACTATAATTACTAGGAATCTAATTTACAG 513

QY 457 gatgggtttgatcttaacaaaggtattgaagcaaaagataaaacacacactcttgcagcacaa 516
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Db 514 GATGGGTTGATCTTAATAAAGGCATTGAAGGAAGATACGTACGCATTGTGCAGGCAT 573
QY 517 tgcacaaatggatcagaaggttagaagttcatgggcagaaactactatttggacatcacca 576
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Db 574 TGTACAAATGGATCAGAAAGTCCATGGATAGAAGCTTCTTATGGGATATCAGAT 633
QY 577 caagaaatcgggaactaaattcaagatatggactgtgata 620
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Db 634 GAAGGAAGTTTGGAAACATAAATTCAGGACATGAAGTGTATATA 677

RESULT 8
US-08-846-344-1
; Sequence 1, Application US/08846344
; Patent No. 6268480
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Filtz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whittters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,344
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
US-08-846-344-1

Query Match 50.2%; Score 311.2; DB 4; Length 1525;
Best Local Similarity 74.8%; Pred. No. 5.3e-77;
Matches 437; Conservative 0; Mismatches 128; Indels 19; Gaps 3;

QY 37 aggaagggaagctcttagagattcttaataatgtctccaaatggagagagaaaaaaag 96
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Db 113 AGGAAGAAAAACAGTAGAGATTCAATTAGTGTCT- - - -AATGTGAAAGAGGACAAAG 168
QY 97 aggcactgtgataattgcctatgataaattcattcttgaagaaacacattatttgagtga 156
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Db 169 AGGCTTTGTGATACTGCTGTGATAATACATTTCTTGAGAAACCATATATTAGTAGA 228
QY 157 aacttcaagattgaattccttgagggaatggctttcattcatttggatgcggtccctc 216
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Db 229 GCTTTTCAGCACACTAAATCCTGGAAATGGCTTT- - - -TGTGCATATCAGATGCTTG 282
QY 217 tataccctgctgttgcacagcatttggctctatgcttctaaatgcctgagataaaagt 276
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Db 283 TGTTCATTCCTTCTTGTACAAATAACTGGCTAT- - - - -TCTTTGGAGATAAAAGTT 333
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Db 334 AATCCTCCTCAGGATTTGAAATATTGGATCCTGGATTAATCTTGGTATCTCTATTGG 393
QY 337 tggcaacctccattatttccgggataattttaaagggaatgcacaaatagaaatgaata 396
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Db 394 TGGAAACCTCCTGTGTATACAAAAATTAAGGGCTGTACACTAGATATCAGTTAAA 453
QY 397 taccgaaacattgtagtgaaactgggaagaccatcaattaccgaaatctacattacaaa 456
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Db 454 TACCGAAATGTTGATAGGCACAGCTGGAAGACTATAATTACTAGGAATCTAATTTACA 513
QY 457 gatgggtttgatcttaacaaaggtattgaagcaaaagataaaacacactcttcgcagc 516
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Db 514 GATGGGTTTGATCTTAATAAAGGCATTGAAGGAAGATACGTACGCATTTGTACAGCAT 573
QY 517 tgcacaaatggatcagaagtttagaagttcatgggcagaaactactatttggacatcac 576
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Db 574 TGTACAAATGGATCAGAAAGTCCATGGATAGAAGCTTCTTATGGGATATCAGAT 633
QY 577 caagaaatcgggaactaaattcaagatatggactgtgata 620
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Db 634 GAAGGAAGTTTGGAACTAAAAATTCAGGACATGAAGTGTATATA 677

RESULT 9
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768

; Sequence 2, Application US/09233086
; Patent No. 6337192
; GENERAL INFORMATION:
; APPLICANT: Bartel, Paul L.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: MMSC1 - An MMAC1 Interacting Protein
; FILE REFERENCE: MMSC1 Gene
; CURRENT APPLICATION NUMBER: US/09/233,086
; CURRENT FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: US 60/071,861
; EARLIER FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5836
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)..(5757)
US-09-233-086-2

Query Match 5.7%; Score 35.2; DB 4; Length 5836;
Best Local Similarity 60.4%; Pred. No. 1.6;
Matches 58; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 520 acaaatggtacgaagtagaagttcattggtggcgaactacttattggaatcacccaa 579
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Db 5646 acgagggatcagatttagctgtaattggtggcgaactggaaggtgttactcagca 5705

QY 580 ggaatcggaacataaaattcaagatgactgt 615
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Db 5706 agcagtcgccattctaaacacacagagggactgt 5741

RESULT 13
US-08-235-836C-71
; Sequence 71, Application US/08235836C
; Patent No. 6248562
; GENERAL INFORMATION:
; APPLICANT: Dunn, John J.
; APPLICANT: Luft, Benjamin J.
; TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
; TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET:
; CITY: Upton
; STATE: NY
; COUNTRY: USA
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,836C
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,191
; FILING DATE: 01-11-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret C.
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: BNL93-28A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 282-7338
; TELEFAX: (516) 282-3729

; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2081 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2081
; US-08-235-836C-71

Query Match 5.6%; Score 34.6; DB 4; Length 2081;
Best Local Similarity 47.8%; Pred. No. 1.6;
Matches 100; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 331 ttgcaatggcaacctccattatttccggataaatttttaaggaatgcacaatagaatgaa 390
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QY 391 ttaaaataccgaaacattgatgtgaaactgggaagaccatcattaccagaatctacat 450
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Db 1150 ATTGAATCAAAAAAGTGATGAAGAACTTTTAAAAAGCAAGATCCTAAAGCATTTAGAT 1209

QY 451 tacaagatgggttggatcttaacaaagggtattgaagcaaaagataaaacacactctgcc 510
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Db 1210 CTTAATCGAGATTAAATTTCTAAAGCTTCTAGTAAAGAAAAATTAAGGCAAGAAAAA 1269

QY 511 gcacaatgcacaaatggatgcagaagttag 539
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Db 1270 GAAATAGTCAAGAGAAATCAAGGTAAG 1298

RESULT 14
US-08-559-896B-1
; Sequence 1, Application US/08559896B
; Patent No. 6310046
; GENERAL INFORMATION:
; APPLICANT: Patrick E. Duffy
; APPLICANT: Christian F. Ockenhouse
; TITLE OF INVENTION: SEQUESTRIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: USA RMC - MCMR-JA
; CITY: FORT DETRICK, FREDERICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,896B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1956 base pairs
; TYPE: Nucleic acid

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 12:24:32 ; Search time 559.18 Seconds
(without alignments)
1903.657 Million cell updates/sec

Title: US-09-828-995b-54

Perfect score: 620

Sequence: 1 ggcacgagctgagtttgtg.....caagatagctggtgtata 620

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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c 2	620	100.0	620	22	Canine interleukin
3	620	100.0	1454	22	Canine interleukin
c 4	620	100.0	1454	22	Canine interleukin
5	437	70.5	1158	22	Canine interleukin
c 6	437	70.5	1158	22	Canine interleukin
7	374	60.3	954	22	Canine IL-13R extr
c 8	374	60.3	954	22	Canine IL-13R extr
9	374	60.3	1095	22	Canine interleukin

c 10	374	60.3	1095	22	AAS59967	Canine interleukin
c 11	374	60.3	1686	22	AAS59970	Canine IL-13R/IgG-
c 12	374	60.3	1686	22	AAS59971	Canine IL-13Ralpha
c 13	374	60.3	1686	22	AAS59976	Canine IL-13R/IgG-
c 14	374	60.3	1686	22	AAS59977	Canine IL-13Ralpha
c 15	374	60.3	1692	22	AAS59974	Canine IL-13R/IgG-
c 16	374	60.3	1692	22	AAS59975	Canine IL-13Ralpha
c 17	374	60.3	1692	22	AAS59972	Canine IL-13R/IgG-
c 18	374	60.3	1698	22	AAS59973	Canine IL-13Ralpha
c 19	341.2	55.0	1289	18	AAT96782	Human zcytor2 cyto
c 20	341.2	55.0	1298	18	AAT86464	Human interleukin-
c 21	341.2	55.0	1298	22	AAT74791	Nucleotide sequenc
c 22	341.2	55.0	1369	18	AAT95214	cDNA encoding the
c 23	341.2	55.0	1369	21	AAA27912	Human interleukin-
c 24	341.2	55.0	1369	21	AAS59991	Human interleukin-
c 25	341.2	55.0	1369	22	AAS59993	Human interleukin-
c 26	341.2	55.0	1369	22	AAD02335	Human interleukin
c 27	341.2	55.0	1369	22	AAC81416	Human IL-13 recept
c 28	338.8	54.6	1288	19	AAV04131	Human HR-1 recepto
c 29	338.8	54.6	1288	19	AAV04075	Human cytokine/pep
c 30	338.8	54.6	1288	19	AAV02295	Homo sapiens cDNA
c 31	324.2	52.3	1126	18	AAT96784	Celebus macaque 2c
c 32	320	51.6	1167	18	AAT96783	Human zcytor2 cyto
c 33	311.2	50.2	1523	18	AAT95213	cDNA encoding the
c 34	311.2	50.2	1523	21	AAA27911	cDNA encoding IL-1
c 35	311.2	50.2	1525	22	AAS59990	Mouse interleukin-
c 36	311.2	50.2	1525	22	AAS59992	Mouse interleukin-
c 37	311.2	50.2	1525	22	AAD02334	Murine interleukin
c 38	311.2	50.2	1525	22	AAC81415	Mouse IL-13 recept
c 39	308	49.7	456	20	AAV89756	EST clone CS520.
c 40	294	47.4	951	24	AAD22980	Human soluble cyto
c 41	293.6	47.4	947	19	AAV22702	Mature interleukin
c 42	293.6	47.4	1079	19	AAV22701	Construct containi
c 43	198.4	32.0	1539	18	AAT85826	Human interleukin-
c 44	192.4	31.0	473	19	AAV22697	Interleukin-13 bin
c 45	74.6	12.0	5311	24	ABL33018	Human immune syste

ALIGNMENTS

RESULT 1

AAS59958

ID AAS59958 standard; cDNA; 620 BP.

XX AC AAS59958;

XX DT 29-JAN-2002 (first entry)

XX Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 620.

XX DE Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;

XX KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG FC;

XX KW Immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;

XX KW Immune response.

XX OS Canis familiaris.

XX XX WO200177332-A2.

XX PN 18-OCT-2001.

XX PD 09-APR-2001; 2001WO-US11498.

XX PF 07-APR-2000; 2000US-195659P.

XX PR 07-APR-2000; 2000US-195874P.

XX PA (HESK-) HESKA CORP.

XX PI McCall CA, Tang L;

XX XX WPI; 2001-657172/75.

XX DR P-PSDB; AAU69133.

XX DR


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Db 440 GGAATGGCTTCATVTCATTTGGATGTCGGATTCCTCTATACCCCTGCTGTTGTCACAGCA 381
Qy 241 ttggctctatgctttcaaatgctgagataaaagtttaactctctcaggaattttgagata 300
Db 380 TTTGGCTCTATGCTTTCAATGCTGAGATAAAAGTTAATCCTCCTCAGGATTTTGAGATA 321
Qy 301 gtggacctggatattaggttatctctctcttgcgaatggcaacctccattatttccggat 360
Db 320 GTGACCCCTGGATATTTAGGTTATCTCTCTTTGCAATGGCAACCTCCATTTATTTCCGGAT 261
Qy 361 aatttaagaatgcacaaatagaatatgaattaaaataccgaacattgatagtgaaac 420
Db 260 AATTTAAGGAATGCACAATAGATAATGAATTAATAATACCGAAACATTGATAGTGAANAAC 201
Qy 421 tgggaagaccatcattaccagaatctacattacaagaatgggtttgattcttaacaaaggt 480
Db 200 TGGGAAGACCATCATTTACCAAGAACTACATTACAAGATGGTTGATCTTAACAAAGGT 141
Qy 481 attgaagcaagaataaacacactctctgcgcgcacaaatgcacaaatgatcagaagttaga 540
Db 140 ATTGAAGCAAGAATAAACACACTTCTGCCAGCACAAATGCCAAATGGATCAGAAAGTTAGA 81
Qy 541 agttcatgggcagaaactactatttgacatcaccacacaaaggaatcgggaaactaaaatt 600
Db 80 AGTTATGGGCAGAAACTACTTATTGGACATCACCAAGGAATCGGAAACTAAAATT 21
Qy 601 caagatatgactgtgtata 620
Db 20 CAAGATATGGACTGTGTATA 1

RESULT 3
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ID AAS59962 standard; cDNA; 1454 BP.
XX AC AAS59962;
XX DT
XX 29-JAN-2002 (first entry)
XX DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1454.
XX KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
XX IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
XX immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX immune response.
XX OS Canis familiaris.
XX PN WO200177332-A2.
XX PD 18-OCT-2001.
XX PF 09-APR-2001; 2001WO-US11498.
XX PR 07-APR-2000; 2000US-195659P.
XX PR 07-APR-2000; 2000US-195874P.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Tang L;
XX WPI; 2001-657172/75.
XX P-PSDB; AAU69135.
XX Novel isolated canine protein, preferably canine immunoglobulin G
XX protein or canine interleukin-13 receptor protein useful for regulating
XX immune response of an animal and for developing regulatory compounds
XX Claim 19; Page 173-175; 22lpp; English.
XX The invention concerns an isolated canine protein, preferably canine
XX immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
```

```
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for developing an immune response in a canine. The proteins are useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
SQ Sequence 1454 BP; 491 A; 238 C; 282 G; 442 T; 1 other;
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Query Match 100.0%; Score 620; DB 22; Length 1454;
Best Local Similarity 100.0%; Pred. No. 1.4e-153;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 241 ttggctctatgctttcaaatgctgagataaaagttaactctctcaggaatttgagata 300
Qy 301 gtgaccttgatattaggttatctctcttgcgaatggcaacctccattatttccggat 360
Db 301 gtgaccttgatattaggttatctctcttgcgaatggcaacctccattatttccggat 360
Qy 361 aattttaagggaatgcacaaatagaatgaattaaataaccgaaacattgtagtgaac 420
Db 361 aattttaagggaatgcacaaatagaatgaattaaataaccgaaacattgtagtgaac 420
Qy 421 tgggaagaccatcattaccagaatctacattacaaagatgggtttgattccttaacaaaggt 480
Db 421 tgggaagaccatcattaccagaatctacattacaaagatgggtttgattccttaacaaaggt 480
Qy 481 attgaagcaagaataaacacacttctccagcacaatgcacaaatggatcagaagttaga 540
Db 481 attgaagcaagaataaacacacttctccagcacaatgcacaaatggatcagaagttaga 540
Qy 541 agttcatgggcagaaactacttatttgacatcaccacaggaataatcgggaaactaaaatt 600
Db 541 agttcatgggcagaaactacttatttgacatcaccacaggaataatcgggaaactaaaatt 600
Qy 601 caagatatggactgtgtata 620
Db 601 caagatatggactgtgtata 620
```

```
RESULT 4
AAS59963/c
ID AAS59963 standard; cDNA; 1454 BP.
XX AC AAS59963;
XX DT 29-JAN-2002 (first entry)
XX DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1454 complement.
```


CC therapy). The present sequence encodes a protein of the invention.

XX Sequence 1158 BP; 380 A; 201 C; 224 G; 353 T; 0 other;

Query Match 70.5%; Score 437; DB 22; Length 1158;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 atggcttcattcattgagatgcgattcctctctataccctgctgttgcacagcattt 243
Db 1 atggcttcattcattgagatgcgattcctctctataccctgctgttgcacagcattt 60
Qy 244 ggctctatgcttcaaaatgcgtgagataaaagttaactcctcctcagatttgagatagtg 303
Db 61 ggctctatgcttcaaaatgcgtgagataaaagttaactcctcctcagatttgagatagtg 120
Qy 304 gacctgcatattaggttatctctcttgcgaatggaacctccattttccggataat 363
Db 121 gacctgcatattaggttatctctcttgcgaatggaacctccattttccggataat 180
Qy 364 tttaagggaatcacaaatagaatgaattaaataaccgaaacattgtagtgaaactgg 423
Db 181 tttaagggaatcacaaatagaatgaattaaataaccgaaacattgtagtgaaactgg 240
Qy 424 aagaccattcattaccagaatctacattacaaagatgggttggatcttaacaaagtatt 483
Db 241 aagaccattcattaccagaatctacattacaaagatgggttggatcttaacaaagtatt 300
Qy 484 gaagcaaaagataaaacacactcttcgcagcaacaatgcacaaatggatcgaaagttagaagt 543
Db 301 gaagcaaaagataaaacacactcttcgcagcaacaatgcacaaatggatcgaaagttagaagt 360
Qy 544 tcattgggcagaaactactatttggacatcacacagaagaatcgaggaaactaaattcaa 603
Db 361 tcattgggcagaaactactatttggacatcacacagaagaatcgaggaaactaaattcaa 420
Qy 604 gatatggactgtgtata 620
Db 421 gatatggactgtgtata 437

RESULT 6
AAS59965/c
ID AAS59965 standard; cDNA; 1158 BP.
XX AC AAS59965;
XX DT 29-JAN-2002 (first entry)
XX DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1158 complement.
XX KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
XX IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
XX immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX immune response.
XX OS Canis familiaris.
XX PN WO200177332-A2.
XX PD 18-OCT-2001.
XX PF 09-APR-2001; 2001WO-US11498.
XX PR 07-APR-2000; 2000US-195659P.
XX PR 07-APR-2000; 2000US-195874P.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Tang L;
XX DR WPI; 2001-657172/75.

XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX Claim 19; Page 179; 221pp; English.
PS The invention concerns an isolated canine protein, preferably canine
XX immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13 proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins are useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX SQ Sequence 1158 BP; 353 A; 224 C; 201 G; 380 T; 0 other;

Query Match 70.5%; Score 437; DB 22; Length 1158;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 atggcttcattcattgagatgcgattcctctctataccctgctgttgcacagcattt 243
Db 1158 atggcttcattcattgagatgcgattcctctctataccctgctgttgcacagcattt 1099
Qy 244 ggctctatgcttcaaaatgcgtgagataaaagttaactcctcctcagatttgagatagtg 303
Db 1098 ggctctatgcttcaaaatgcgtgagataaaagttaactcctcctcagatttgagatagtg 1039
Qy 304 gacctgcatattaggttatctctcttgcgaatggaacctccattttccggataat 363
Db 1038 gacctgcatattaggttatctctcttgcgaatggaacctccattttccggataat 979
Qy 364 tttaagggaatgcacaaatagaatgaattaaataaccgaaacattgtagtgaaactgg 423
Db 978 tttaagggaatgcacaaatagaatgaattaaataaccgaaacattgtagtgaaactgg 919
Qy 424 aagaccattcattaccagaatctacattacaaagatgggttggatcttaacaaagtatt 483
Db 918 aagaccattcattaccagaatctacattacaaagatgggttggatcttaacaaagtatt 859
Qy 484 gaagcaaaagataaaacacactcttcgcagcaacaatgcacaaatggatcgaaagttagaagt 543
Db 858 gaagcaaaagataaaacacactcttcgcagcaacaatgcacaaatggatcgaaagttagaagt 799
Qy 544 tcattgggcagaaactactatttggacatcacacagaagaatcgaggaaactaaattcaa 603
Db 798 tcattgggcagaaactactatttggacatcacacagaagaatcgaggaaactaaattcaa 739
Qy 604 gatatggactgtgtata 620
Db 738 gatatggactgtgtata 722

RESULT 7
AAS59968
ID AAS59968 standard; cDNA; 954 BP.
XX AC AAS59968;
XX DT 29-JAN-2002 (first entry)
XX DE Canine IL-13R extracellular domain cDNA nCaIL-13Ralpha2 954.
XX KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;

KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.

OS Canis familiaris.

XX WO200177332-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001WO-US11498.

XX 07-APR-2000; 2000US-195659P.

XX 07-APR-2000; 2000US-195874P.

XX (HESK-) HESKA CORP.

XX McCall CA, Tang L;

XX WPI; 2001-657172/75.

XX P-PSDB; AAU69137.

XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -

XX Claim 19; Page 184-185; 221pp; English.

XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.

XX Sequence 954 BP; 329 A; 162 C; 192 G; 271 T; 0 other;

Query Match 60.3%; Score 374; DB 22; Length 954;

Best Local Similarity 100.0%; Pred. No. 7.7e-89;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 tctatgctttcaaaagtctgagataaaagttaattctctcctcaggattttgagatagtgac 306

DB 4 tctatgctttcaaaagtctgagataaaagttaattctctcctcaggattttgagatagtgac 63

QY 307 cctgcatatttaggttatctctcttgcaatggcaatggcaacctcattttccggataatttt 366

DB 64 cctgcatatttaggttatctctcttgcaatggcaatggcaacctcattttccggataatttt 123

QY 367 aaggaatgcacaaatgaatatgaattaaataaccgaacattgtagtgaacactgggaag 426

DB 124 aaggaatgcacaaatgaatatgaattaaataaccgaacattgtagtgaacactgggaag 183

QY 427 accatcattaccagaatctacattacaaagatgggtttgtattcttcaacaaaggtattgaa 486

DB 184 accatcattaccagaatctacattacaaagatgggtttgtattcttcaacaaaggtattgaa 243

QY 487 gcaagataaaacacactctgcagacacaaatgcacaaatggatcagaagttgaagtcca 546

DB 244 gcaagataaaacacactctgcagacacaaatgcacaaatggatcagaagttgaagtcca 303

QY 547 tgggcagaaactcattattggacatcaccacaaagaaatcgggaaactaaattcaagat 606

DB 304 tgggcagaaactcattattggacatcaccacaaagaaatcgggaaactaaattcaagat 363

QY 607 atggactgtgtata 620
DB 364 atggactgtgtata 377

RESULT 8

AAS59969/C

XX AAS59969 standard; cDNA; 954 BP.

XX AAS59969;

XX 29-JAN-2002 (first entry)

XX Canine IL-13R extracellular domain cDNA nCaIL-13Ralpha2 954 complement.

XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;

XX IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;

XX immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX immune response.

XX Canis familiaris.

XX WO200177332-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001WO-US11498.

XX 07-APR-2000; 2000US-195659P.

XX 07-APR-2000; 2000US-195874P.

XX (HESK-) HESKA CORP.

XX McCall CA, Tang L;

XX WPI; 2001-657172/75.

XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -

XX Claim 19; Page 187; 221pp; English.

XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.

XX Sequence 954 BP; 271 A; 192 C; 162 G; 329 T; 0 other;

Query Match

Best Local Similarity 60.3%; Score 374; DB 22; Length 954;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 tctatgctttcaaaagtctgagataaaagttaattctctcctcaggattttgagatagtgac 306

DB 951 TCTATGCTTCAAAATGCTGAGATAAAAGTTAATCTCTCTCAGGATTTTTCAGATAGTGAC 892

QY 307 cctgcatatttaggttatctctcttgcaatggcaatggcaacctcattttccggataatttt 366

DB 891 CCTGGATATTTAGGTATTCTCTTTGCAATGGCAACCTCCATTATTTCCGGATAATTTT 832

Qy 367 aaggaatgcacaataagaatatgaattaaataaccgaaacattgatagtgaaactggaag 426
 Db 831 AAGGAATGCACAATAGAAATATGAATTAATAATACCGAAACATGTATGATGAAACCTGGAG 772
 Qy 427 accatcattaccagaactctcatcattacaaagatgggtttgatcttaacaaaggtattgaa 486
 Db 771 ACCATCATTACCAGAATCTACATTACAAAGATGGTTTGATCTTAACAAGGTATTGAA 712
 Qy 487 gcaagataaacacacactctccagcacaatgcacaaatggatcagaagttagaagtcca 546
 Db 711 GCAAGATAAACACACTTCTGCCAGCACAATGCACAAATGGATCAGAAGTTAGAAGTTCA 652
 Qy 547 tgggcagaaactactatttgacatcaccacaaagaaatcgggaaactaaattcaaat 606
 Db 651 TGGGCAGAAACTACTATTATTGGACATCACCAAGGAATCGGAAACTAAAAATTCAGAT 592
 Qy 607 atggactgtgata 620
 Db 591 ATGGACTGTGTATA 578
 RESULT 9
 AAS59966
 ID AAS59966 standard; cdna; 1095 BP.
 XX
 AC AAS59966;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1095.
 XX
 KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.
 XX
 OS Canis familiaris.
 XX
 PN WO200177332-A2.
 XX
 PD 18-OCT-2001.
 XX
 XX 09-APR-2001; 2001WO-US11498.
 PF
 XX 07-APR-2000; 2000US-195659P.
 PR
 PR 07-APR-2000; 2000US-195874P.
 XX
 XX (HESK-) HESKA CORP.
 PA
 XX McCall CA, Tang L;
 PI
 XX WPI; 2001-657172/75.
 DR
 DR P-PSDB; RAU69136.
 XX
 PT Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -
 XX
 PS Claim 19; Page 179-181; 221pp; English.
 CC
 CC The invention concerns an isolated canine protein, preferably canine
 CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
 CC receptor protein, the nucleic acids encoding them, antibodies
 CC raised against them, fusion proteins between the IgG and IL-13R proteins
 CC and methods of isolating regulators of them. The regulators are useful
 CC for regulating an immune response in a canine. The proteins useful to
 CC develop regulatory compounds including inhibitors and activators that,
 CC when administered to a canine in an effective manner, are capable of
 CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
 CC regulators are useful for treating canine IgG (heavy and/or light chain)
 CC and/or canine IL-13R mediated responses. The molecules of the invention
 CC are useful to regulate the immune response of an animal (e.g. by gene
 CC therapy). The present sequence encodes a protein of the invention.

XX SQ Sequence 1095 BP; 370 A; 186 C; 211 G; 328 T; 0 other;
 Query Match 60.3%; Score 374; DB 22; Length 1095;
 Best Local Similarity 100.0%; Pred. No. 8e-89;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 247 tctatgcttcaaaatgctgagataaaagttaactctctcagcagattttgagatagtggaac 306
 Db 1 tctatgcttcaaaatgctgagataaaagttaactctctcagcagattttgagatagtggaac 60
 Qy 307 cctggaatttaggttatctctcttgcgaatgcgaacacctccattttcccgataatttt 366
 Db 61 cctggaatttaggttatctctcttgcgaatgcgaacacctccattttcccgataatttt 120
 Qy 367 aaggaatgcacaataagaatatgaattaaataaccgaaacattgatagtgaaactggaag 426
 Db 121 aaggaatgcacaataagaatatgaattaaataaccgaaacattgatagtgaaactggaag 180
 Qy 427 accatcattaccagaactctcatcattacaaagatgggtttgatcttaacaaaggtattgaa 486
 Db 181 accatcattaccagaactctcatcattacaaagatgggtttgatcttaacaaaggtattgaa 240
 Qy 487 gcaagataaacacacactctccagcacaatgcacaaatggatcagaagttagaagtcca 546
 Db 241 gcaagataaacacacactctccagcacaatgcacaaatggatcagaagttagaagtcca 300
 Qy 547 tgggcagaaactactatttgacatcaccacaaagaaatcgggaaactaaattcaaat 606
 Db 301 tgggcagaaactactatttgacatcaccacaaagaaatcgggaaactaaattcaaat 360
 Qy 607 atggactgtgata 620
 Db 361 atggactgtgata 374
 RESULT 10
 AAS59967/c
 ID AAS59967 standard; cdna; 1095 BP.
 XX
 AC AAS59967;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1095 complement.
 XX
 KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.
 XX
 OS Canis familiaris.
 XX
 PN WO200177332-A2.
 XX
 PD 18-OCT-2001.
 XX
 XX 09-APR-2001; 2001WO-US11498.
 PF
 XX 07-APR-2000; 2000US-195659P.
 PR
 PR 07-APR-2000; 2000US-195874P.
 XX
 XX (HESK-) HESKA CORP.
 PA
 XX McCall CA, Tang L;
 PI
 XX WPI; 2001-657172/75.
 DR
 DR Novel isolated canine protein, preferably canine immunoglobulin G
 DR protein or canine interleukin-13 receptor protein useful for regulating
 DR immune response of an animal and for developing regulatory compounds -
 XX

```
PS Claim 19; Page 183; 221pp; English.
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX Sequence 1095 BP; 328 A; 211 C; 186 G; 370 T; 0 other;

Query Match 60.3%; Score 374; DB 22; Length 1095;
Best Local Similarity 100.0%; Pred. No. 8e-89;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 tctatgctttcaaaatgctgagataaaaagttaatcctctcctcaggtatttgagataggac 306
Db TCTATGCTTTCAAATGCTGAGATAAAAAGTTAATCCTCTCCTCAGGATTTGAGATAGTGGAC 1036

QY 307 cctggatatttaggttatctctcttgcgaatggcaacctccattattccggataatttt 366
Db CCTGGATATTTTAGGTTATCTCTCTTGCAAATGGCAACCTCCATTATTTCCGGATAATTTT 976

QY 367 aaggaatgcacaatagaatgaattaaataaccgaacattgatgtgaaaaactggaag 426
Db AAGGAATGCACAATAGATATGAATTAATAATACCGAACAATTGATGACTGAAAACCTGGGAAG 916

QY 427 accatcattaccagaatctacattacaaaagatgggtttgatctcttaacaaagttatgaa 486
Db ACCATCATTTACCAAGAATCTACATTACAAAGATGGTTTGATCTTTAAACAAGGTATTGAA 856

QY 487 gcaagataaaacacacctctgcgcagcacaaatgcacaaatggatcagaagttagaagtcca 546
Db GCAAGATAAAACACACACTTCTGCGCAGCAAAATGCACAAATGGATCAGAAGTTAGAAGTTCA 796

QY 547 tgggcagaaactacttatttggacatcaccaagaagaaatcgggaaactaaattcaagat 606
Db TGGGCAGAAACTACTTATTGGACATCACCAACAAGGAATCGGGAACATAAAATTCAAGAT 736

QY 607 atggactgtgtata 620
Db ATGGACTGTGTATA 722

RESULT 11
AAS59970
ID AAS59970 standard; cDNA; 1686 BP.
XX
AC AAS59970;
XX
XX 29-JAN-2002 (first entry)
XX
XX Canine IL-13R/IgG-Fc fusion protein cDNA nCaIL-13Ralpha2-Fc3523 1683.
XX
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
XX WO200177332-A2.
XX
XX 18-OCT-2001.
XX
XX
```

```
XX 09-APR-2001; 2001WO-US11498.
PF
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI; 2001-657172/75.
DR P-PSDB; AAU69138.
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX Claim 37; Page 187-190; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
XX Sequence 1686 BP; 513 A; 384 C; 382 G; 407 T; 0 other;

Query Match 60.3%; Score 374; DB 22; Length 1686;
Best Local Similarity 100.0%; Pred. No. 9.2e-89;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 tctatgctttcaaaatgctgagataaaaagttaatcctctcctcaggtatttgagataggac 306
Db TCTATGCTTTCAAATGCTGAGATAAAAAGTTAATCCTCTCCTCAGGATTTGAGATAGTGGAC 63

QY 307 cctggatatttaggttatctctcttgcgaatggcaacctccattattccggataatttt 366
Db CCTGGATATTTTAGGTTATCTCTCTTGCAAATGGCAACCTCCATTATTTCCGGATAATTTT 123

QY 367 aaggaatgcacaatagaatgaattaaataaccgaacattgatgtgaaaaactggaag 426
Db AAGGAATGCACAATAGATATGAATTAATAATACCGAACAATGATGAGAAACCTGGAAG 183

QY 427 accatcattaccagaatctacattacaaaagatgggtttgatctcttaacaaagttatgaa 486
Db ACCATCATTTACCAAGAATCTACATTACAAAGATGGTTTGATCTTTAAACAAGGTATTGAA 243

QY 487 gcaagataaaacacacctctgcgcagcacaaatgcacaaatggatcagaagttagaagtcca 546
Db GCAAGATAAAACACACACTTCTGCGCAGCAAAATGCACAAATGGATCAGAAGTTAGAAGTTCA 303

QY 547 tgggcagaaactacttatttggacatcaccaagaagaaatcgggaaactaaattcaagat 606
Db TGGGCAGAAACTACTTATTGGACATCACCAACAAGGAATCGGGAACATAAAATTCAAGAT 363

QY 607 atggactgtgtata 620
Db ATGGACTGTGTATA 377

RESULT 12
AAS59971/C
ID AAS59971 standard; cDNA; 1686 BP.
XX
```



```
Db      4 tctatgctttcaaatgctgagataaaagttaatactctctcctcaggattttgagatagtgac 63
Qy      307 cctgatatattaggttatctctcttgcgaatggaacccctccatttcccgataatttt 366
Db      64 cctgatatattaggttatctctcttgcgaatggaacccctccatttcccgataatttt 123
Qy      367 aaggaaatgcacaataagaatgaataaaataccgaacacacattgagtgaaaactgggaag 426
Db      124 aaggaaatgcacaataagaatgaataaaataccgaacacacattgagtgaaaactgggaag 183
Qy      427 accatcattaccagaatctacattaccagaatgaggtgttgatctcttaacaaaggattttaa 486
Db      184 accatcattaccagaatctacattaccagaatgaggtgttgatctcttaacaaaggattttaa 243
Qy      487 gcaaaagataaaacacactctcgcagcacacaatgcacaaatggatcagaagttagaagtcca 546
Db      244 gcaaaagataaaacacactctcgcagcacacaatgcacaaatggatcagaagttagaagtcca 303
Qy      547 tgggcagaaactactatttggacatcacaccacaggaatacgggaaactaaaattcaaat 606
Db      304 tgggcagaaactactatttggacatcacaccacaggaatacgggaaactaaaattcaaat 363
Qy      607 atggactgtgtata 620
Db      364 atggactgtgtata 377

RESULT 14
AAS59977/c
ID      AAS59977 standard; cDNA; 1686 BP.
XX
AC      AAS59977;
XX
DT      29-JAN-2002 (first entry)
XX
DE      Canine IL-13Ralpha2/IgG-Fc fusion protein cDNA reverse complement #4.
XX
KW      Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
KW      IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW      immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX      immune response.
XX      Canis familiaris.
XX      WO200177332-A2.
XX      18-OCT-2001.
XX
PF      09-APR-2001; 2001WO-US11498.
XX
PR      07-APR-2000; 2000US-195659P.
PR      07-APR-2000; 2000US-195874P.
XX
PA      (HESK-) HESKA CORP.
XX
PI      McCall CA, Tang L;
XX
DR      WPI; 2001-657172/75.
XX
PT      Novel isolated canine protein, preferably canine immunoglobulin G
PT      protein or canine interleukin-13 receptor protein useful for regulating
PT      immune response of an animal and for developing regulatory compounds -
XX
PS      Claim 37; Page 212-213; 221pp; English.
XX
CC      The invention concerns an isolated canine protein, preferably canine
CC      immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC      receptor protein, the nucleic acids encoding them, antibodies
CC      raised against them, fusion proteins between the IgG and IL-13 proteins
CC      and methods of isolating regulators of them. The regulators are useful
CC      for regulating an immune response in a canine. The proteins useful to
CC      develop regulatory compounds including inhibitors and activators that,
```

```
CC      when administered to a canine in an effective manner, are capable of
CC      protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC      regulators are useful for treating canine IgG (heavy and/or light chain)
CC      and/or canine IL-13R mediated responses. The molecules of the invention
CC      are useful to regulate the immune response of an animal (e.g. by gene
CC      therapy). The present sequence is the reverse complement of a cDNA
XX      encoding a protein of the invention.
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SQ Sequence 1686 BP; 407 A; 379 C; 388 G; 512 T; 0 other;

Query Match 60.3%; Score 374; DB 22; Length 1686;
Best Local Similarity 100.0%; Pred. No. 9.2e-89;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1443 gcaaaagataaaacacactctcgcagcacacaatgcacaaatggatcagaagttagaagtcca 1384
Qy      547 tgggcagaaactactatttggacatcacaccacaggaatacgggaaactaaaattcaaat 606
Db      1383 tgggcagaaactactatttggacatcacaccacaggaatacgggaaactaaaattcaaat 1324
Qy      607 atggactgtgtata 620
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RESULT 15
AAS59974
ID AAS59974 standard; cDNA; 1692 BP.

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AC      AAS59974;
XX
DT      29-JAN-2002 (first entry)
XX
DE      Canine IL-13R/IgG-Fc fusion protein cDNA nCaIl-13Ralpha2-Fc-B9 1689.
XX
KW      Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
KW      IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW      immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX      immune response.
XX
OS      Canis familiaris.
XX
PN      WO200177332-A2.
XX
PD      18-OCT-2001.
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PF      09-APR-2001; 2001WO-US11498.
XX
PR      07-APR-2000; 2000US-195659P.
PR      07-APR-2000; 2000US-195874P.
XX
PA      (HESK-) HESKA CORP.
XX
PI      McCall CA, Tang L;
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XX WPI; 2001-657172/75.
DR P-PSDB; AAU69140.
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX Claim 37; Page 200-203; 221pp; English.
XX
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13alpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
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XX Sequence 1692 BP; 518 A; 376 C; 385 G; 413 T; 0 other;
SQ

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Query Match 60.3%; Score 374; DB 22; Length 1692;
Best Local Similarity 100.0%; Pred. No. 9.3e-89;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 307 cctggataattaggttattctctcttgcattggcaacctccattatttccggataatttt 366
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Db 124 aaggaatgcacaatagatatgaattaaataccgaaacattgatagtgaaaactgggaag 183
Qy 427 accatcattaccaagaattcattacaaagatgggtttgatcttaacaaaggatttgaa 486
Db 184 accatcattaccaagaattcattacaaagatgggtttgatcttaacaaaggatttgaa 243
Qy 487 gcaaaagataaacacacttctgccagcacaaatgcacaaatgatcagaagttagaagtcca 546
Db 244 gcaaaagataaacacacttctgccagcacaaatgcacaaatgatcagaagttagaagtcca 303
Qy 547 tgggcagaaactacttattgacatccaccagaagaatcggaataactaaaaattcaagat 606
Db 304 tgggcagaaactacttattgacatccaccagaagaatcggaataactaaaaattcaagat 363
Qy 607 atggactgtgtata 620
Db 364 atggactgtgtata 377

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Job time: 17338 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 11:31:47 ; Search time 5720.3 Seconds
(without alignments)
2268.142 Million cell updates/sec

Title: US-09-828-995B-54

Perfect score: 620

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

AX280319

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

CDS

linear PAT 02-NOV-2001

620 bp DNA

AX280319 Sequence 54 from Patent WO0177332.

AX280319

AX280319.1 GI:16607697

dog.

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (sites)

McCall, C.A. and Tang, L.

Compositions and methods related to canine igg and canine il-13

receptors

Patent: WO 0177332-A 54 18-OCT-2001;

Heska Corporation (US)

Location/Qualifiers

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/db_xref="taxon:9615"

184..>618

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BASE COUNT 212 a 102 c 127 g 179 t
ORIGIN

Query Match 100.0%; Score 620; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 2e-127;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGCACAGGCTGAGTTGTGTGCTTGATTATCAGACAGAGGGAAGGCTTTAGAGATTCT 60
Qy 61 aattaatgtctccaaactggagaagaaaaaaagagagacctgtgataattgcctatga 120
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Db 361 AATTTAAAGGAATGCACAAATAGAATATCAATTAATAATACCGAAACATTTGATGTAAGAAC 420
Qy 421 tggagaaccatcattaccagaatctacattacaagaatgggttgattctttaacaaagt 480
Db 421 TGGAGAACCATCATTTACCAAGAATCTACATTACAAAGATGGGTTTGATCTTTAACAAAGGT 480
Qy 481 attgaagcaagataaacaacactctccagcacacatacacaaaatggatcagaagttaga 540
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Qy 601 caagatatggactgtgtata 620
Db 601 CAAGATATGGACTGTGTATA 620

RESULT 2
AX280321/c
LOCUS AX280321 620 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 56 from Patent WO0177332.
ACCESSION AX280321
VERSION AX280321.1 GI:16607699
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13

receptors
Patent: WO 0177332-A 56 18-Oct-2001;
Heska Corporation (US)
Location/Qualifiers
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source 1. .620
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/db_xref="taxon:9615"
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Best Local Similarity 100.0%; Pred. No. 2e-127;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ggcacagagctgagttgtgtgcttgattatcagacagagaagggaagctcttagagattct 60
Db 620 GGCACAGGCTGAGTTGTGTGCTTGATTATCAGACAGAGGGAAGGCTTTAGAGATTCT 561
Qy 61 aattaatgtctccaaactggagaagaaaaaaagagagacctgtgataattgcctatga 120
Db 61 AATTAAATGCTCCAAACTGGAGAGAGAAAAAAGAGACCTGTGATAATTGCCCTATGA 501
Qy 121 taattcattcttggagaaccatattattgagtggaacctcaaaagcttgaattcttggga 180
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Db 200 TGGAGAACCATCATTTACCAAGAATCTACATTACAAAGATGGGTTTGATCTTTAACAAAGGT 141
Qy 481 attgaagcaagataaacaacactcttgcagcacacatacgacaaaatggatcagaagttaga 540
Db 140 ATTGAAGCAAAAGATAAACACACTTCTGCCAGCACAAATGCACAAATGGATCAGAAGTTAGA 81
Qy 541 agttcatgggcagaactacttattggacatcacacagaagaaatcgggaaactaaaatt 600
Db 80 AGTTTCATGGCAGAAACTTACTTATTGGACATCACCACAAGGAATTCGGGAACATAAATT 21
Qy 601 caagatatggactgtgtata 620
Db 20 CAAGATATGGACTGTGTATA 1

RESULT 3
AF314533
LOCUS AF314533 1454 bp mRNA linear MAM 16-OCT-2001
DEFINITION Canis familiaris interleukin 13 receptor alpha chain 2 (IL13Ra2)
ACCESSION AF314533
VERSION AF314533.1 GI:16151870
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1454)

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Qy 421 tggagaccatcatcattaccaagaattacattacaagaatgggtttgatcttacaagaagt 480
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Db 421 TCGAAGACCATCATTTACCAAGAATCTACATTTACAAGAATGGGTTTGATCTTTAACAAAGGT 480
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Qy 481 attgaagcaagataaaacacactctctgccagacacaatagcacaaatggatgaagttaga 540
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Qy 541 agttcatgggcagaaactacttatttggacatcacacaggaatacggggaactaaaatt 600
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Qy 601 caagatatggactgtgtata 620
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RESULT 5
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DEFINITION Sequence 62 from Patent WO0177332.
ACCESSION AX280327
VERSION AX280327.1 GI:16607705
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE McCall,C.A. and Tang,L.
JOURNAL Compositions and methods related to canine igg and canine il-13
Patent: WO 0177332-A 62 18-OCT-2001;
HEska Corporation (US)
FEATURES
source
1. .1454
/organism="Canis familiaris"
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BASE COUNT 442 a 282 c 238 g 491 t 1 others
ORIGIN

Query Match 100.0%; Score 620; DB 6; Length 1454;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 63 from Patent WO0177332.
ACCESSION AX280328
VERSION AX280328.1 GI:16607706
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE McCall,C.A. and Tang,L.
JOURNAL Compositions and methods related to canine igg and canine il-13
Patent: WO 0177332-A 63 18-OCT-2001;
HEska Corporation (US)
FEATURES
source
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BASE COUNT 380 a 201 c 224 g 353 t
ORIGIN

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Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 TCATGGCGAGAACTACTTATTGGACATCACCAAGAAATCGGGAACCTAAAAATTCAA 420
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Qy 604 gataggactgtgtata 620
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RESULT 7
AX280329/c
LOCUS AX280329 1158 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 64 from Patent WO0177332.
ACCESSION AX280329
VERSION AX280329.1 GI:16607707
KEYWORDS
SOURCE
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 64 18-OCT-2001;
Heska Corporation (US)
FEATURES
source Location/Qualifiers
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/organism="Canis familiaris"
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BASE COUNT 353 a 224 c 201 g 380 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.9e-87;
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Qy 304 gacctggtatttaggttactctctcttgcaatggcaacctccattatttccggataat 363
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Qy 424 aagaccatcattaccagaactctacattacaaagatgggttttgatcttaacaaaggtatt 483
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RESULT 8
AX280333
LOCUS AX280333 954 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 68 from Patent WO0177332.
ACCESSION AX280333
VERSION AX280333.1 GI:16607711
KEYWORDS
SOURCE
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 68 18-OCT-2001;
Heska Corporation (US)
FEATURES
source Location/Qualifiers
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Db 184 ACCATCATTTACCAAGAACTACATTACAAGATGGTTGATCTTTAACAAGGTATTGAA 243
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Qy 487 gcaagaataaacacacactctcctcagacacaatgcagaaatgagatcagaagttagaagtca 546
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Db 244 GCAAGATTAACACACTTCTGCCAGCACAAATGCACAAATGGATCAGAAAGTTAGAAGTTCA 303
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Db 304 TGGCGAGAACTACTTATTGGACATCACCAAGAAATCGGGAACCTAAAAATTCAAGAT 363
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Qy 607 atggactgtgtata 620
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JOURNAL Patent: WO 0177332-A 67 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:9615"
BASE COUNT 328 a 211 c 186 g 370 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.3e-73;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 607 atggactgtgtata 620
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RESULT 12
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LOCUS AX280336 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 71 from Patent WO0177332.
ACCESSION AX280336
VERSION AX280336.1 GI:16607714
KEYWORDS
SOURCE doq.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 71 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5e-73;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 73 from Patent WO0177332.
ACCESSION AX280338
VERSION AX280338.1 GI:16607716
KEYWORDS
SOURCE doq.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 73 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
source 1..1686
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/db_xref="taxon:9615"
BASE COUNT 407 a 382 c 384 g 513 t
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Query Match 60.3%; Score 374; DB 6; Length 1686;
Best Local Similarity 100.0%; Pred. No. 5e-73;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX280345 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 80 from Patent WO0177332.
ACCESSION AX280345
VERSION AX280345.1 GI:16607723
KEYWORDS
SOURCE
ORGANISM
dog.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS
1 (sites)
McCall,C.A. and Tang,L.
TITLE
Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL
Patent: WO 0177332-A 80 18-OCT-2001;
Heska Corporation (US)
LOCATION/Qualifiers
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BASE COUNT 512 a 388 c 379 g 407 t
ORIGIN

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RESULT 15
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LOCUS AX280347 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 82 from Patent WO0177332.
ACCESSION AX280347
VERSION AX280347.1 GI:16607725
KEYWORDS
SOURCE
dog.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS
1 (sites)
McCall,C.A. and Tang,L.
TITLE
Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL
Patent: WO 0177332-A 82 18-OCT-2001;
Heska Corporation (US)
LOCATION/Qualifiers
FEATURES
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RESULT 14
AX280345
LOCUS AX280345 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 80 from Patent WO0177332.
ACCESSION AX280345
VERSION AX280345.1 GI:16607723
KEYWORDS
SOURCE
ORGANISM
dog.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS
1 (sites)
McCall,C.A. and Tang,L.
TITLE
Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL
Patent: WO 0177332-A 80 18-OCT-2001;
Heska Corporation (US)
LOCATION/Qualifiers
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Query Match 60.3%; Score 374; DB 6; Length 1686;
Best Local Similarity 100.0%; Pred. No. 5e-73;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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Title: US-09-828-995B-57

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 9	262.6	29.9	517	9	AW136614
C 10	252	28.7	365	9	AA298563
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C 12	233.8	26.6	506	9	AW236406
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20	180.6	20.6	403	10	BG201950
21	180.4	20.5	409	10	BG215092
C 22	178	20.3	360	9	AA621766
C 23	171	19.5	823	10	BF968964
C 24	164.6	18.7	465	10	BF523126
C 25	158.2	18.0	446	9	AW001800
C 26	150.4	17.1	465	10	R52796
C 27	147.2	16.8	658	10	BI828427
C 28	133.4	15.2	755	10	BE619361
C 29	128.2	14.6	341	9	AA921043
C 30	87.4	10.0	160	9	AI547789
C 31	84.8	9.7	530	12	AZ557979
C 32	69.6	7.9	176	12	AZ108580
C 33	58	6.6	1101	12	CNS0039G
C 34	58	6.6	1201	12	CNS016E1
C 35	54.2	6.2	469	12	AQ761600
C 36	53.2	6.1	987	12	CNS014FQ
C 37	53	6.0	928	12	CNS00DKY
C 38	52.8	6.0	1043	12	CNS0145P
C 39	52	5.9	1101	12	CNS00EVL
C 40	50.8	5.8	928	12	CNS00DKY
C 41	50.6	5.8	1200	12	CNS016CO
C 42	49.8	5.7	1101	12	CNS016L1
C 43	49.2	5.6	1101	12	CNS0039G
C 44	49	5.6	1101	12	CNS016TX
C 45	49	5.6	1201	12	CNS007JU

ALIGNMENTS

RESULT 1
AL562513/c
LOCUS AL562513 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC012YF21 3 prime, mRNA sequence.
ACCESSION AL562513
VERSION AL562513.1 GI:12911007
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 928)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .928
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC012YF21"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

FEATURES
source

BASE COUNT 265 a 186 c 158 g 312 t 7 others


```

Db 196 TTAATATTAGTATTATTGTAACCGGTCTGCTTTTGGGTAGCCAAACCCCTACCCAAAA 137
Qy 715 acgat-----ctttcatacaaaaaaagagtcttttcttccatcaacagacattctgttg 767
Db 136 ATGATCCAGAAATTTTCTGTGATACATGAAGACTTTCCATATCAAGAGACATGCTATTG 77
Qy 768 actcagtaacttttcagctcttatgccagatgtttaaatatgatgttattataaactgaagct 827
Db 76 ACTCAACAGTTTCCAGTC--ATGCCCAAAATGTTCAATATGAGTCTCAATAAATGAATTT 19
Qy 828 ttctctcaaatattgaa 844
Db 18 TTATAACGAATGTGAA 2

RESULT 3
AL525497
LOCUS AL525497 LTI_NFL003_NBC3 954 bp mRNA linear EST 13-FEB-2001
DEFINITION AL525497 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC012YF21 5
prime, mRNA sequence.
ACCESSION AL525497
VERSION AL525497
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 954)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 954
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC012YF21"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 295 a 172 c 201 g 285 t 1 others
ORIGIN

Query Match 40.4%; Score 354.4; DB 9; Length 954;
Best Local Similarity 84.0%; Pred. No. 4.4e-50;
Matches 400; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 1 caaggaatcgggaactcaaatcaagatatgactgtgtatattacaaactggcaatat 60
Db 474 CAAGGAATTCAGAAACTAAAGTTTCAGGATATGATGCGTATATATACAAATGGCAATAT 533
Qy 61 ttactgtctcttggaaacctggcatgggtgtccattttgatataccaattaccagttgttt 120
Db 534 TTACTGTCTTCTGGAAACCTGGCATAGGTGTACTTCTTGATACCAATATCAACTTGTGT 593
Qy 121 tactggtatagggcttggaccatccagcagagtgctactgattacatacaaggttaatgga 180
Db 594 TACTGGTATGAGGGCTTGGATCATGCATACAGTGTGTGTGATTACATCAAGGCTGATGGA 653

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Qy 181 aaaaatgggatcgaggtttccctattttggagtcatacagactataaagattttcacatc 240
Db 654 CAAAATATAGGATCGAGATTTCCCTATTTTGGAGGCATCAGACTATAAAGATTTCATATAT 713
Qy 241 tgtttaatgggtcatcagaatccagcctatccagccatcagaccagctatttttttttcagctt 300
Db 714 TGTGTTAATGGATCATCAGAGAAAGCCATATCAGATCAGTTATTTTTCACTTTCAGCTT 773
Qy 301 caaaatatagttaaacctatgccaccagactacaccttagctcttactgtgaaagaatttcagag 360
Db 774 CAAAATATAGTTAAACCTTTGCCGCCAGCTCTATCTTACTTTTACTCGGAGAGTTTCATGT 833
Qy 361 gaaattaaccttgaaatggaaacatgcctaaaggacccattccagcccaaatgttttcatttat 420
Db 834 GAAATTAAGCTGAAATGGAGCATACCTTTGGGACCTATTCCAGCAAGGTGTGTTTGATTAT 893
Qy 421 gaaattgaattcacagagagtggtactacttctgggtgactaccacagttggagaatga 476
Db 894 GAAATTGAGATCAGAGAAGATGATACTACCTTGGTGACTGCTACAGTTTGAAATGA 949

RESULT 4
BE620022/c
LOCUS BE620022
DEFINITION BE620022 926 bp mRNA linear EST 20-OCT-2000
601473366T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876064 3',
mRNA sequence.
ACCESSION BE620022
VERSION BE620022.1 GI:98909060
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 926)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM9636 row: d column: 17
High quality sequence start: 26
High quality sequence stop: 704.

FEATURES
source
1. 926
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3876064"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 271 a 186 c 169 g 300 t
ORIGIN

Query Match 39.7%; Score 349; DB 10; Length 926;
Best Local Similarity 75.5%; Pred. No. 3.6e-49;
Matches 567; Conservative 0; Mismatches 165; Indels 19; Gaps 10;

Qy 39 tgtattatacaactggcaatttttagtctctctctggaaacctggcagctgggtgtccattt 98
Db 764 TCCGTATATTACTATGCCAAATATTACTCTGTTCTTGG-AAACCTGGAATAGGTGTACTGTC 706

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found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM9783 row: 1 column: 23
 High quality sequence stop: 677.

FEATURES

source

1..867
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4212574"
 /clone_lib="NCI_CGAP_Brn64"
 /tissue_type="glioblastoma with EGFR amplification"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Brain; Vector: pCMV-SPT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.57 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

277 a 155 c 199 g 236 t

BASE COUNT

ORIGIN

Query Match 35.3%; Score 310.2; DB 10; Length 867;
 Best Local Similarity 74.7%; Pred. No. 1.1e-42;
 Matches 486; Conservative 0; Mismatches 148; Indels 17; Gaps 7;

QY 208 ttggagtcacagactaaagattttacatctgtgttaatgggtcatcagaatccacg 267
 Db 56 TTGGAGGCATCAGACTAAAGATTTCTATATTTGTGTAAATGTCATCAGAGAACAAG 115

QY 268 cctacagaccagctatttttttcagcttcaaaatagtagtaaacctatgccacca 327
 Db 116 CCTATCAGATCCAGTTATTTACATTTTCAGCTTCAAAATAGTTAAACCTTTGCCGCCA 175

QY 328 gactacaccttagcttactgtgaagaattcagaggaataacacctgaatggaacatgcct 387
 Db 176 GTCTATCTTACTTCGGGAGAGTCTATGTCGAATTAAGCTGAATGAGCATACCT 235

QY 388 aaaggaccattccagccaaatgtttcatttatgaattgaattcagagggatggtact 447
 Db 236 TTGGAGCCTATTCCAGCAAGGTGTTGA-TTATGAAATTCAGATCAGAGAAGATGATACT 294

QY 448 acttggtgactaccaggtggaatgagatcacaaatcacagaacatcaaatggaagc 507
 Db 295 ACCTTGCTGACTGCTACAGTTTGAAGATGAACATACACCTTTGAAACAAACAAATGAAC 354

QY 508 caaaattatgcttttggtaagaagtaaaagtgaattttattgtctcagatgatggaatc 567
 Db 355 CGACAATTATGCTTTGTAGTGAAGCAAGTGAATATTTA-TGCTCAGATGACGGAAT 413

QY 568 tggagtgagtgagtgatgaacaatgctggaaggt---gacatatggaaggaacacctta 624
 Db 414 TGGAGTGAGTGGAGTATAACAATGCTGGGAAGGTGAAGACCTTATCGAAGAAAACCTTG 473

QY 625 gtattttcttgataccattgtcttctcatttctcaattttgttggtaataactgctg 684
 Db 474 CTACGTTCTGCGCTACCATTTGGTTTCATCTTAATATAGTTAT-ATTGTAACCGGCTG 532

QY 685 cttttgtatagaaggaagggctttactgaaaacgat-----ctttcatcaaaaaaaga 737
 Db 533 CTTTTCGTTAGCCAAACACCTACCCAAATGATTCAGAAATTTTCTGTGATACATGA 592

QY 738 agtctttctcatcaagacacattctgttactcagtaactttcagttcttatggccagat 797
 Db 593 AGACTTGCCATATCAGCAGACATGGTATTGACTC---AACAGTTCCAGTCATGGCCAAAT 649

QY 798 gttaaatatgagctttattaaactgaagcttttctcctcaaatatgaataaa 848
 Db 650 G-TCATATGAGTCTCAATACTGGATTTCTTGGAAAAAATAAAAAA 699

RESULT 7

AW629184/c

LOCUS

DEFINITION h152b02.x1 Soares_NFL_T_GBC_s1 Homo sapiens cdna clone

579 bp mRNA linear EST 31-MAR-2000

IMAGE:2975883 3' similar to SW:1132_HUMAN Q14627 INTERLEUKIN-13
 RECEPTOR ALPHA-2 CHAIN PRECURSOR ;, mRNA sequence.

AW629184
 AW629184.1 GI:7375974

FEATURES

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 579)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -400P from Gibco

High quality sequence stop: 284.

Location/Qualifiers

1..579

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2975883"

/clone_lib="Soares_NFL_T_GBC_s1"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Equal amounts of plasmid DNA from three normalized

libraries (fetal lung NBHL19W, testis NHT, and B-cell

NCI_CGAP_GCB1) were mixed, and ss circles were made in

vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from pools of 5,000 clones made

from the same 3 libraries. The pools consisted of

I.M.A.G.E. clones 297480-302087, 682632-687239,

726408-728711, and 729096-731399. Subtraction by Bento

Soares and M. Fatima Bonaldo.

BASE COUNT 177 a 109 c 107 g 186 t

ORIGIN

Query Match 33.1%; Score 291; DB 9; Length 579;

Best Local Similarity 73.3%; Pred. No. 2.1e-39;

Matches 417; Conservative 0; Mismatches 140; Indels 12; Gaps 3;

QY 271 atcagaccagctattttttttcagcttcaaaatagtttaaacctatgccaccagac 330

Db 579 ATCAGATCATGTCATTTCTTTATCAGCTTCAAGATATAGTTACACCTCCGCCGCTC 520

QY 331 taccttagcttactgtgaagaattcagaggaataacacctgaatggaacatgcctaaa 390

Db 519 CATGTTCAATTTTACTCGGAGAGTTCATGTCGAATTCAGCTGAATGGAGCATACCTTTG 460

QY 391 ggaccattccagccaaatgtttcatttatgaaattgaaattcacagaggtggtactact 450

Db 459 GCACCTATTCCAGCAAGGTGTTTGATTATGAAATTTAGATCAGAGAAGATGATACCTACC 400

QY 451 tgggtgactacacagttgagaatgagatatacaaaatcaacaagaacatcaaaatgaagccaa 510

Db 399 TTGGTACTGTATACAGTTGAAATGAAACATACACCTTTGAAACAAACAAATGAAACCCGA 340

QY 511 aaattatgcttttggtaagaagtaaaagtgaattattattctcagatgaggaatctgg 570

Db 339 CAATTATGCTTTGTAGTGAAGCAAGCAAGTGAATATTTATTGCTCAGATGACGGAATTTGG 280

QY 571 agtgagtgagtgatgaacaatgctggaaggt---gacatatggaaggaacaccttagta 627

Db 279 AGTGAGTGGAGTGAATAACATGCTGGGAAGGTGAAGACCTATCGAAGAAACCTTTGCTA 220

QY 628 ttttcttgatcaccatttgcctttgtctcaatattgttttgggttaataactgctgctt 687

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Db 219 CGTTCTCGCTACCAATTTGGTTTCATCTTAATATTAGTATTATATTGTAACCGGTGCTT 160
Qy 688 ttgtataagcaaggcgtttactgaaacagat-----ctttcatcaacaaaaagaagt 740
Db 159 TTGCGTAAGCCAAACACCTACCCAAAATGATTCAGAAATTTTCTGTGATACATGAAGA 100
Qy 741 cttttctctcaagaacacatctgttgactcagtaaccttccagtcatttgccagatgtt 800
Db 99 CTTTCCATATCAAGAGACATGTAATGACTCAACAGATTTCAGTC--ATGCCAAATGTT 42
Qy 801 aaatatgagtgcttattaaactgaagcttt 829
Db 41 CAATATAAATCTCCATAAACTGAATTTT 13

RESULT 8
BF591502/c 537 bp mRNA linear EST 30-MAR-2001
LOCUS nab99a12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3275807 3'
DEFINITION similar to SW:II32_HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2
CHAIN PRECURSOR ; mRNA sequence.
ACCESSION BF591502
VERSION BF591502.1 GI:11683826
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 537)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 480.
FEATURES
Location/Qualifiers
1..537
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3275807"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site1: Not I; Site2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGCGCGGCATATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 161 a 108 c 94 g 170 t 4 others
ORIGIN
Query Match 32.6%; Score 286.6; DB 10; Length 537;
Best Local Similarity 74.8%; Pred. No. 1.2e-38;
Matches 400; Conservative 0; Mismatches 123; Indels 12; Gaps 3;
Qy 307 atagttaacctatgccaccagctacctagtcttactgtgaagaattcagaggaaatt 366
|||||

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Db 537 ATAGTTAAACCTTTGCCGCCAGTCTATCTTACTTTTACTCGGGAGAGTTTCATGTGAATT 478
Qy 367 aacctgaatggaacatgcctaaagacccattccagcaaatgtttcatattatgaatt 426
Db 477 AAGCTGNAATGGAGCANACCTTTGGGACCTATTCAGCAAGGTGTTTGATTATGAATT 418
Qy 427 gaattcacagagagtggtactacttgggtgactcacacagttgagaatgagatacaaatc 486
Db 417 GAGATCAGAGAAGATGATACCTTGGTNGCTGTACAGTTGAAATGAAACACACACC 358
Qy 487 acaagaacatcaaatgaaagccaaataattgtcttttggtaagaagtaaatgtaatt 546
Db 357 TTGAAAACAACAATGAAACCCGACAATTATGCTTTGTAGTAAGAAGCAAAAGTGAATAT 298
Qy 547 tattgctcagatgatgaatcgtgagtgagtgagtgatgaacaatgctggaaggt--- 603
Db 297 TATTCTCAGATGACGGAATTTGGAGTGAGTGGAGTGATAAACAATGCTGGGAAGGTGAA 238
Qy 604 gacatatgaaagaaacaccttagtattttcttgatcaccattgtcttctcgaattt 663
Db 237 GACCTATCGAAGAAACCTTGTCTAGCTTCTGCTACCATTTGGTTTCATCTTAATTA 178
Qy 664 gtttgggtaaaccttgctgctgtttgtatagaagcaagggtttactgaaacagat--- 719
Db 177 GTTATATTTGTAACCGGTCTGCTTTTGGCTAAGCCAAACACCTACCCAAAATGATCCA 118
Qy 720 ---ctttcatcaacaaaaagaagtcttttctcacaagacacattctgttgactcagtaa 776
Db 117 GAATTTTCTGTGANACATGAAGACTTTCATATCAAGAGACATGGTATTGACTCAACAG 58
Qy 777 ctttcactgttatggccagatgttaaatgagctgtcttataaactgaagcttttc 831
Db 57 TTTCCAGTC--ATGCCCAAATGTTCAATATGAGTCTCAATAAATGAAATTTTCC 5

RESULT 9
AW136614/c 517 bp mRNA linear EST 29-OCT-1999
LOCUS UI-H-B11-aco-g-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
DEFINITION IMAGE:2715080 3', mRNA sequence.
ACCESSION AW136614
VERSION AW136614.1 GI:6140747
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 517)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. CDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
Location/Qualifiers
1..517
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2715080"
/clone_lib="NCI_CGAP_Sub3"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site1: Not I; Site2: Eco RI; The
NCI_CGAP_Sub3 library is a subtracted library derived from

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the NCI_CGAP_Sub1 library, which is a subtracted library derived from Br. 41 constitutes a mixture of 21 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Le12, NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6, NCI_CGAP_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:

NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonids 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonids 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE Clonids 1414920-1417991, 1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonids 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonids 983608-986759, 1101192-1101359, 1217928-1220615); NCI_CGAP_Co10 pool 1 LLAM 2844-2653, 2871-2872 (IMAGE Clonids 1057416-1061255, 1144584-1145351). Subtraction was performed as previously described [Bonaldi, Lennon & Soares (1996)]: Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

TAG_L1B-NCI_CGAP_Lu5
TAG_TISSUE-lung
TAG_SEQ=CAAC"

BASE COUNT	150 a	102 c	84 g	181 t
ORIGIN				

Query Match	29.9%;	Score 262.6;	DB 9;	Length 517;
Best Local Similarity	73.6%;	Pred. No. 1.2e-34;		
Matches 379;	Conservative 0;	Mismatches 124;	Indels 12;	Gaps 3;
Qy	344	ctgtgaagaattcagagaaataacctgaaatgaacatgcctaaaggacccattccag	403	
Db	517	CTCGGAGAGTTCATGTGAATAATGACTAAATGGAGCATACCTTTGGGAGCTATTCCAG	458	
Qy	404	ccaaattgttctattgaattgaattccagaggaagggtactactctgggtgactaccca	463	
Db	457	CAAGGTGTTTGATTGAAATTGAGATCAGAGAAGATGATACATACCTTGGTACTGCTA	398	
Qy	464	cagtgagaatgagatcacaaatcacagaagacatcaaatgaaagccaaaaattatgctttt	523	
Db	397	CAGTTGAAAATGAAACATACACCTTGAAAAACAACAAATGAAACCCGACAAATTATGCTTTG	338	
Qy	524	tggtaagaagtaaaagtgaattatttctgcagatgatggaatctggaagtgaagtggadtg	583	
Db	337	TAGTAAGAAGCAAAAGTGAATATTTATTGCTCAGATGACGGAAATTTGGAGTCAAGTGGAGTG	278	
Qy	584	atgaacaatgctggaaaggt---gacatatggaaggaacaccttagtatctttcttgatcac	640	
Db	277	ATAACAATGCTGGAGGTGAAGACCTATTCGAAGAAACCTTTCGTACGTTTCGGCTTAC	218	
Qy	641	catttgcctttgtctcaatatgttttggtaaaccttgcctgctgtttgtataaagcaaa	700	
Db	217	CATTTCGTTTCATCTTAATATTAGTTATATTGTTAAACGGTCTGCTTTTGGCTAAGCCAA	158	
Qy	701	gggtcttactgaaacagat-----ctttcatacaaaaaaagaagcttttcttcatac	753	
Db	157	ACACCTACCCCAAAATGATTCAGAAATTTTCTGTGATACATGAAGACTTTCCTCATATCAA	98	
Qy	754	gacacattctgttgaactcagtaacttcagtccttatggccagatggttaaatatagctctt	813	
Db	97	GAGACATGGTATTGACATCAACAGTTTCCAGTTC---ATGGCCAAATGTTTCAATATGAGTCTC	40	

Qy	814	attaactgaagccttttccctaataattgaaataaa	848
Db	39	AATAAAGCTGAATTTTCTTGCGAAAAA	5

RESULT	10
AA298563	
LOCUS	EST14178 HSC172 cells I Homo sapiens cDNA 5' end similar to IL13 receptor (IL13R), mRNA sequence.
DEFINITION	
ACCESSION	AA298563
VERSION	AA298563.1 GI:1950896
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 365)
	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Frichman,J.L., Geophagen,N.S., Glodek,A., Gehrm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrier,A., Fischer,A., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., HungJun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE	96026280
COMMENT	Other_ESTs: THC194124 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse. Location/Qualifiers 1. 365 /organism="Homo sapiens" /db_xref="ATCC (inhost):178283" /db_xref="taxon:9606" /clone_lib="HSC172 cells I" /cell_type="fibroblast" /cell_line="HSC172 (16PDL)" /dev_stage="fetal" /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI ; Site_2: XhoI"
FEATURES	
source	
BASE COUNT	106 a 66 c 69 g 123 t 1 others
ORIGIN	

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Query Match      28.7%  Score 252;  DB 9;  Length 365;
Best Local Similarity 86.1%;  Pred. No. 8.3e-33;
Matches 290;  Conservative 0;  Mismatches 46;  Indels 1;  Gaps 1;

Qy 1 caaggaaatcgggaaactaaaattcaaagataggactgtgtattatacaactggcaaat 60
    15 CAAGGAATTCAGAAACTTAAAGTTCAGAGATATGGATTGCGTATATTACAAATTGGCAATAT 74
Db 15 CAAGGAATTCAGAAACTTAAAGTTCAGAGATATGGATTGCGTATATTACAAATTGGCAATAT 74

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QY 61 ttagtctgcttggaaacctggcatgggtgccatttggatcaccaattaccagttgttt 120
Db 75 TTACTCTGTTCTTGGAAACCTGGCATAGGTGACTCTTTGATACCAATTACAACCTGTTT 134
QY 121 tactggtatgagggcttgaccattcagcagagtgtagctgattacatcaaggttaatgga 180
Db 135 TACTGGTATGAGGGCTTGGTATGATGATACGATTTACAGTGTGTGATTATACATCAAGGCTGATGGA 194
QY 181 aaaaatatggatgcaggtttccctatttggagtcacatcagactataaaagatttctacac 240
Db 195 CAAAATATAGGATGTCAGATTTCCCTATTGAGGATCATCAGATATAAAGATTTCTATATT 254
QY 241 tctgtaattgggtcatcagaatcccgacctatcacaccagctatttta-tttttcagct 299
Db 255 TGTGTTAATGGATCATCAGAGNCAAGCCTATCAGATCCAGTATTTCACCTTTTCCAGCT 314
QY 300 tcaaatatagttaaacctatgccaccagactacett 336
Db 315 TCAAAATATAGTTAAACCTTTGCCGCCAGCTCTATCCT 351

RESULT 11
BE788633 715 bp mRNA linear EST 20-OCT-2000
LOCUS 601475992F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878831 5',
DEFINITION mRNA sequence.
ACCESSION BE788633
VERSION BE788633.1 GI:10209831
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 715)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9643 row: g column: 24
High quality sequence stop: 575.
FEATURES
Location/Qualifiers
1..715
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3878831"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 229 a 154 c 141 g 191 t
ORIGIN

Query Match 26.9%; Score 236.6; DB 10; Length 715;
Best Local Similarity 76.1%; Pred. No. 2.4e-30;
Matches 372; Conservative 0; Mismatches 104; Indels 13; Gaps 6;

QY 1 caaggaatccggaactaaattcaagataggactgtgtatattacaaactggaatat 60
Db 195 CAAGGAATCCAGAACTAAAGTTTCAGGATATGGATTGCTATATTACAAATGGCAATAT 254

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QY 61 ttagtctgcttggaaacctggcatgggtgccatttggatcaccaattaccagttgttt 120
Db 255 TTACTCTGTTCTTGGAAACCTGGCATAGGTGACTCTTTGATACCAATTACAACCTGTTT 314
QY 121 tactggtatgagggcttgaccattcagcagagtgtagctgattacatcaaggttaatgga 180
Db 315 TACTGGTATGAGGGCTTGGATCATGATGATACGATTTACAGTGTGTGATTATACATCAAGGCTGATGGA 374
QY 181 aaaaatatggatgcaggtttccctatttggagtcacatcagactata-aagattttcaca- 238
Db 375 CAAAATATAGGATGTCAGATTTCCCTATTGAGGATCATCAGATATAAAGATTTCTATATC 434
QY 239 ---tctgttaattgggtcatcagaatcccgacctatcacaccagctatttt-tattttt 294
Db 435 TTTGCTGTTTACACTGATCATCAGAGAACAGCCTATCAGATCCAGTATTATTTCCACTTTT 494
QY 295 cagcttcaaa---atatagttaaacctatgccaccagactaccttagtcttactgtgaag 351
Db 495 CAGCTTCAAAACATATACGCTTAAACCTATGCCGCCAGTCTATCTTACTTTAAACTCGGGAG 554
QY 352 aattcagaggaataaactgaaatggaacatgcctctaaagga---ccattccagccaaa 408
Db 555 AGTTTCATGTGAATTAAGCTGACATGGGAGCATACACGAGACCTATCCACCAGGT 614
QY 409 tgttcatttatgaattgaattcacagaggtggtgactacttggtg-actaccacagt 467
Db 615 GCTACCGATCATGACATTCGGATCAGAGAAGATGATACCTCTGCTGACTGCTACAGT 674
QY 468 tgagaatga 476
Db 675 CGAAATATGA 683

RESULT 12
AW236406/c
LOCUS AW236406
DEFINITION x015g12.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2704102 3',
similar to SW:1132_HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2
CHAIN PRECURSOR ;, mRNA sequence.
ACCESSION AW236406
VERSION AW236406.1 GI:6568795
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 506)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -400p from gibco
High quality sequence stop: 407.
FEATURES
Location/Qualifiers
1..506
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2704102"
/clone_lib="NCI_CGAP_Ut2"
/cisue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"

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/lab_host="DH10B"
/Note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
BASE COUNT      151 a      105 c      84 g      166 t
ORIGIN

Query Match      26.6%; Score 233.8; DB 9; Length 506;
Best Local Similarity 74.3%; Pred. No. 8e-30;
Matches 365; Conservative 0; Mismatches 112; Indels 14; Gaps 5;

Qy 363 aattaacctgaatggaacatgcctaaaggagcccaattccagccaaattttcattatga 422
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 487 AATTAAAGCTGAATGGAGCAACCCCT-TGGGACCTATTCCAGCAAGGTGTTTGATTATGA 429

Qy 423 aatgaattcacagaggatgactactactctggtgactaccacagtggaatgagataca 482
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 428 AA-TGAGATCAGAGAAGATGATACCTTGGTGACTGTACAGTTGAGATGAACATA 370

Qy 483 aatcacaagaacatacaaatgaaagcgaataattgcttttggtaagaagtaaaagtga 542
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 369 CACCTTGAACACAAATGAACCCGACATATATGCTTTGTAGTAAGACCAAGTGA 310

Qy 543 tatttattgctcagatggaatctgagtgagtgagtgagtgagtgagtgagtgagtgag 602
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 309 TATTTATTGCTCAGATACGGAATTTGGAGTGAGTGAGTGAACAAATGCTGGGAAG 250

Qy 603 t---gacatatggaaggaacaccttagtatttttcttgataccattgtttgtctcaat 659
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 249 TGAAGACCTTGAAGAAACCTTTCGTACGTTCTGGCTACCATTTGGTTTCATCTTAAT 190

Qy 660 atttttttggtaataaactgctgctcttggtaagaagggctttactgaaacagat 719
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 189 ATTACTTATATTGTAACCGGCTGCTTTTGGTAAGCAACACACTACCCCAAAATGAT 130

Qy 720 -----cttttcatacaaaaaaagtgctttcttcatacaagacacactctgttgactca 772
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 TCCAGAAATTTTCTGTGATACATGAAGACTTTCCATATATCAAGAGACATGGTATTGACTCA 70

Qy 773 gtaacttcagctcttatggcagatgttaaatatagctcttataaactgaagcttttcc 832
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 ACAGTTTCCAGTC--ATGGCCAAATGTTCAATATGAGTCTCAATAACTGAATTTTCTT 12

Qy 833 tcaaatattga 843
      ||||| |||||
Db 11 GCGAATGTAA 1

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RESULT 13
AI358911/c      479 bp      mRNA      linear      EST 15-FEB-1999
LOCUS          qy19c05.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2012456 3'
DEFINITION     similar to SW:1132_HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2
CHAIN          CHAIN PRECURSOR ; , HUMAN sequence.
ACCESSION      AI358911
VERSION        AI358911.1 GI:4110532
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 479)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
REFERENCE      National Cancer Institute / National Institute of Neurological
AUTHORS        Disorders and Stroke, Brain Tumor Genome Anatomy Project
TITLE          (CGAP/BTGP), Tumor Gene Index
JOURNAL        Unpublished (1998)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                Ph.D.

```

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1039 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 324.

FEATURES
 Location/Qualifiers
 1..479
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 /db_xref="taxon:9606"
 /clone="IMAGE:2012456"
 /clone_lib="NCI_CGAP_Brn23"
 /tissue_type="glioblastoma (pooled)"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCCGCATATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
 BASE COUNT 144 a 98 c 79 g 157 t
 ORIGIN

Query Match 26.4%; Score 231.4; DB 9; Length 479;
 Best Local Similarity 73.7%; Pred. No. 2.1e-29;
 Matches 351; Conservative 0; Mismatches 112; Indels 13; Gaps 4;

Qy 364 attaacctgaaatgaaacatgcctaaaggagcccaattccagccaaattttcattatga 423
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 479 ATTAAGCTGAATGGAGCAT-ACTTTGGGCCCTATCCAGCAAGGTGTTTGTATTGATGAN 421
Qy 424 attgaattcacagaggatggtactctggtgactaccacagtgagatgagataca 483
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 420 ATTGAGATCAGAGAAGATGATACCTTGGTGACTGTACAGTTGAAATGGAACATAC 361
Qy 484 atcacaagaacatcaaatgaaagcccaaaatattgcttttggtaagaagtaaaagtga 543
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 360 GCCTTGAAACAAACAAATGAAACCCGACAAATATGCTTTGTAGTAAGAGCAAGTGAAT 301
Qy 544 atttattgctcagatgagaaatctgagtgagtgagtgagtgagtgagtgagtgagtg 603
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 300 ATTTATTGCTCAGATGACGGAATTTGGAGTGAGTGAGTGAACAAATGCTGGGAAGGT 241
Qy 604 ---gacatatggaaggaacaccttagtattttcttgataccattgttcttcaata 660
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 240 GAAGACCTATCAAGAAACTTTGTACGTTTCTGGCTACCATTTGGTTTCATCTTAATA 181
Qy 661 ttgttttggtaataaactgctgcttttggtaagaagggcttttactgaaacgat- 719
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 TTAGTTATATTGTAACCGGCTGCTTTTGGCTAAGCCAAACACCTTACCCAAAATGATT 121
Qy 720 -----cttttcatacaaaaaaagagcttttcttcatacaagacacattctgtgactc 773
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 CCAGAAATTTTCTGTGATACATGAAGACTTTCCATATCAAGAGACATGGTATTGACTCAA 61
Qy 774 taacttcagctcttatggcagatgttaaatagctcttataaactgaagctttt 829
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 CAGTTTCCAGTC--ATGGCCAAATGTTCAATATGAGTCTCAATAAATGAATTTT 7

RESULT 14
 AA909507/c
 LOCUS AA909507
 DEFINITION olitedil.sl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:1523637 3' similar to SW:1132_HUMAN Q14627 INTERLEUKIN-13

```
RECEPTOR ALPHA-2 CHAIN PRECURSOR ;, mRNA sequence.
AA909507
VERSION AA909507.1 GI:3048912
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 443)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 609 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 220.
Location/Qualifiers
1. 443
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1523637"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
BASE COUNT 134 a 88 c 74 g 147 t
ORIGIN
Query Match 26.2%; Score 230; DB 9; Length 443;
Best Local Similarity 74.8%; Pred. No. 3.6e-29;
Matches 332; Conservative 0; Mismatches 100; Indels 12; Gaps 3;
QY 399 tcacgcaaatgttttcatttatgaaattcagagaggtggtactacttgggtgac 458
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 443 TCCAGCAAGGTGTTTGATTGAAATGAGATCAGAGAAGATGATACCTTGGTGAC 384
QY 459 taccacagtgtgagatgagatcaaatcaagaacatcaaatgaaagccaaattatg 518
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 383 TCGTACAGTTGAAATGAACATACACCTTGAACACAAATGAACCCGCAATATG 324
QY 519 ctttttggtaagaagtaaagtgaattatttctcagatgatggaatctggagtgg 578
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 323 CTTTGTAGTAAAGCAAGCAAAAGTGAATATTTATTGCTCAGATACGGAATTTGGAGTGAGTG 264
QY 579 gagtgtgaacaatgctggaagggt---gacatatggaaggaaaccttagtattttctt 635
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 263 GAGTGATAAACAAATGCTGGGAAGGTGAAGACCTATCGAAGAAACCTTCTACGTTTCG 204
QY 636 gataccatttcttctcctcattttgttggtaataacttgcctgtcttggatataa 695
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 203 GCTACCATTTGGTTTCATCTTAATATAGTTATATTTGTAACCGGTCCTCTTTGGGTAA 144
QY 696 gcaagggttcttactgaaacagat-----ctttcatacaaaaaaagaagctcttctc 748
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 143 GCCAAACACCTACCCAAAAATGATCCAGAAATTTTCTGTGATACATGAAGACTTTCCAT 84
QY 749 atcaagacacattctgttgactcagtaactttcagctcttcttgccagagcttaaatatga 808
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 83 ATCAGAGACATGGTATTGACTCAACAGTTTCCAGTC--ATGGCCAAATGTTCAATATGA 26
QY 809 gcttattaaactgaagcttttcc 832
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LOCUS BE964459/c
DEFINITION BE964459
ACCESSION BE964459
VERSION BE964459
KEYWORDS EST.
SOURCE BE964459.2 GI:11767928
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 675)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Oct 3, 2000 this sequence version replaced gi:10575164.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/Dnp/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC623 row: d column: 17
High quality sequence stop: 654.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3876064"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 199 a 133 c 145 g 198 t
ORIGIN
Query Match 25.4%; Score 223.2; DB 10; Length 675;
Best Local Similarity 70.4%; Pred. No. 4.2e-28;
Matches 472; Conservative 0; Mismatches 173; Indels 25; Gaps 12;
QY 198 gtttcctcattggagctcagactataaagattctctacatctgtgtaattgggtc 257
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QY 258 agaattcccgctatcagaccagctattttatttcagcttcaaaatatagttaaacc 317
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DB 606 AGAGACA-AGCCTATCAGATCCGG-TATTTACCTTTCAGCTTCCAAATATAGTGAACC 549
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QY 437 aggatgttactacttgggtgactacca-cagttgagaatgagatacaaaatcaagaaca 495
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Qy 549 ttgct-cagatgatggaatctggagtgagtgagtgatgaacaatgctggaaaagt----g 604
Db 310 TTGCTCCAGATGACGGAAATTTGGAGTGAGTGGAGTGATAAACCATGCTGGGAAGGTGAAG 251
Qy 605 acatatgaaggaacacctagatttttcttgataccatttgcttttctcacaatatitg 664
Db 250 ACCATCGAAGAAACTTTGCTACGTTTCTGGCTACCCCTTTGGTTTCATCTTAATATTAG 191
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Result No.	Query			ID	Description
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	2	533.6	60.8	1369	4 US-08-841-751-3 Sequence 3, Appli
	3	533.6	60.8	1369	4 US-08-846-340-3 Sequence 3, Appli
	4	533.6	60.8	1369	4 US-08-846-344-3 Sequence 3, Appli
	5	446	50.8	1525	1 US-08-609-572-1 Sequence 1, Appli
	6	446	50.8	1525	4 US-08-841-751-1 Sequence 1, Appli
	7	446	50.8	1525	4 US-08-846-340-1 Sequence 1, Appli
	8	446	50.8	1525	4 US-08-846-344-1 Sequence 1, Appli
	9	42.2	4.6	7218	1 US-08-233-463-14 Sequence 14, Appli
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	15	38.4	4.4	3355	4 US-09-136-828-3 Sequence 3, Appli
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	17	37.4	4.3	1241	1 US-07-593-657-6 Sequence 6, Appli
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	20	37	4.2	854	4 US-08-998-416-534 Sequence 534, App
	21	37	4.2	860	4 US-08-998-416-287 Sequence 287, App
	22	37	4.2	1472	4 US-08-781-420-10 Sequence 10, Appl
23	37	4.2	1472	4 US-08-781-420-12 Sequence 12, Appl	
24	37	4.2	1472	4 US-08-874-102-10 Sequence 10, Appl	
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Query Match 60.8%; Score 533.6; DB 1; Length 1369;
Best Local Similarity 78.9%; Pred. No. 4.4e-126;
Matches 677; Conservative 0; Mismatches 169; Indels 12; Gaps 3;

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Db 739 TGTGTATTATGGATCATCAGAAACGCTATCAGATCCAGTATTTCACTTTTCAGCTT 798
Qy 301 caaataatagtttaaacctatgccaccagactacccttagtcttactgtgaagaattcagag 360
Db 799 CAAATATAGTTAAACCTTTCGCCGCCAGTCTATCTTACTTTTACTCGGAGAGTTTCATGT 858
Qy 361 gaaataacctgaaatggaacatgctctaaaggaccatccagcgaatgttttcattat 420
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RESULT 2
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; Sequence 3, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
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; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
; US-08-841-751-3
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Query Match 60.8%; Score 533.6; DB 4; Length 1369;
Best Local Similarity 78.9%; Pred. No. 4.4e-126;
Matches 677; Conservative 0; Mismatches 169; Indels 12; Gaps 3;

Qy 1 caaggaaatcgggaaactaaattcaagatatggaactgtgatatatacaactggcaaat 60
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RESULT 3
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; Sequence 3, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
; US-08-846-340-3
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Query Match 60.8%; Score 533.6; DB 4; Length 1369;
Best Local Similarity 78.9%; Pred. No. 4.4e-126;

Matches 677; Conservative 0; Mismatches 169; Indels 12; Gaps 3;

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Qy 1 caaggaatcgggaaactcaaatcaagatatgactgtgtatattacaactggcaatat 60
Db 499 CAAGGAATTCAGAAACTAAAGTTCAGGATATGATTGCGTATATTACAATTTGCAATAT 558
Qy 61 ttactgtctcttggaaacctgggcatgggtgccattttgtatataccaaattaccagttgtt 120
Db 559 TTACTCTGTTCTTGGAAACCTGGCATAGTGTACTTCTTGATACCAATTTACAACCTTGTTT 618
Qy 121 tactgggtatgaggcttgaccattcagcagagtgactgattaccatcaagggttaatgga 180
Db 619 TACTGGTATGAGGGCTTGGATCATGCAATTACAGTGTGTGTTGATTACATCAAGGCTGATGA 678
Qy 181 aaaaatggtgatcaggtttccctatttggagtcacagactataaagatttctcacatc 240
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Qy 241 tgtgttaatgggtcatcagaatcccagcctatccagaccagctattttatttttcagctt 300
Db 739 TGTGTTAATGGATCATCAGAGAACAAGCCTATCAGATCCAGTTATTTCACATTTTTCAGCTT 798
Qy 301 caaatatagttaaacctatgccaccagactacacttactgtgagaatccaag 360
Db 799 CAAAATATAGTTAAACCTTTGCCGCCAGTCTATCTACTTTTTCCTCGGGAGAGTTTCTGT 858
Qy 361 gaaattaaacctgaaatggaacatgcctaaagagccattccagccaaatgtttcatttat 420
Db 859 GAAATTAAAGCTGAAATGGAGCATACCTTTGGGACCTATTCCAGCAAGGTGTTTTCATAT 918
Qy 421 gaaattgaattcacagaggtggttactacttgggtgactaccacagttgagaatgagata 480
Db 919 GAAATTGAGATCAGAGAAGATGATACCTTGGTGGTACTGCTACAGTTGAAATGAAACA 978
Qy 481 caaatcacaagaacatcaaatgaaagccaaaaattatgcttttgggtaagaagttaaagt 540
Db 979 TACACCTTGAAACAAACAATGAAACCCGACAAATATGCTTTGTAGTAAGAAGCAAAAGT 1038
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Db 1039 AATATTATTGCTCAGATGAGCGGAATTGGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAG 1098
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; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
; US-08-609-572-1

Query Match 50.8%; Score 446; DB 1; Length 1525;
Best Local Similarity 71.5%; Pred. No. 6.3e-104;
Matches 631; Conservative 0; Mismatches 241; Indels 11; Gaps 3;

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Db 635 AAGGAAGTTTGAAACTAAATTCAGGACATGAAGTGTATATATTATACTGGCAGTATT 694

Qy 62 tagtctcttgaacctggcgtgggtccatttggatcaccaattaccagttgttt 121
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Db 695 TGGTCTGCTCTGGAAACCTGGCAAGACAGTATATCTGTACCAACTATACCATGTGTTT 754

Qy 122 actggtatgagggcttgaccattcagcagagtgactgattacatcaagggttaagtga 181
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Db 755 TCTGTATGAGGCTTGGATCATGCTTACAGTGTGCTGATTACCTCCAGCATGATAA 814

Qy 182 aaatatggatgcagggttccctatttggagtcacagactataaagatttctacatct 241
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Qy 242 gtgttaatgggtcatcagaatccagccctatcagaccagctatttttttcagcttc 301
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 875 GTGTTAATGGATCTTCAAAGTTGGAACCCATCAGATCAGCTATACAGTTTTCACATTC 934

Qy 302 aaatatagttaaacctatgcaccagactaccttagtcttactgtgaagaattcagagg 361
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 935 AAAATATAGTTAAACCATTGGCACCAGAAATTCCTTCATATAGTGTGAGAAATTCATG 994

Qy 362 aaattaacctgaatggaactgacctaaagaccattccagccaaatgtttcattttatg 421
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 995 ATATTAGAATGAATGGAGCACACCTCGGAGGACCCATTCACCAAGGTTTACACTTATG 1054

Qy 422 aaattgaattcacagagatggtactacttgggtgactaccacagttgagaatgagatc 481
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1055 AAATGTGTCGGAAGAACCATATTTCTGGGAGTCTCCACAGACAAAACGATATGA 1114

Qy 482 aaatcacagaactcaaatgaaagccaaataattatgcttttggtaagaagtaagtga 541
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1115 AGTTGAAGGAGAGCAAAATGAAGTGAAGACCTATGCTTTTGTAGATGTAAGGTCA 1174

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US-08-841-751-1

Query Match 50.8%; Score 446; DB 4; Length 1525;
Best Local Similarity 71.5%; Pred. No. 6.3e-104;
Matches 631; Conservative 0; Mismatches 241; Indels 11; Gaps 3;

Qy 2 aaggaatcgggaactaaattcaagatatgagctggtgtatattacaaactggcaatt 61
Dbb 635 AAGGAAGTTTGGAACTAAATTCAGGACATGAAGTGATATATATTAACGGCAGTATT 694
Qy 62 tagtctgctctggaaactggcctggtgtccattttgataccaaactaccagttgttt 121
Dbb 695 TGGTCTGCTCTTGGAACTGCGAAGACAGATATATCTGTATACCAACTATACCATGTTTT 754
Qy 122 actggtatgagggctggaccattcagcagagtgctactgattacatcaagggttaattgaa 181
Dbb 755 TCTGGTATGAGGGCTTGGATCATGCTTACAGTGTGCTGATTTACCTCCAGCATGATGAAA 814
Qy 182 aaaaatgggagtcaggggttccctatttggagtcacagactataaagattttcacatct 241
Dbb 815 AAAATGTTGGATGCAAACTGTCCAATGGACTGGACTCATCAGACTATAAAGATTTTTTATCT 874
Qy 242 gttttaaattgggtcatcagaatcccagccctatcagaccagctatttttttcagcttc 301
Dbb 875 GTGTTAAATGGATCTTCAAAGTTTGGAACTGAGATCCAGATCCAGCTATACAGTTTTTCAACTTC 934
Qy 302 aaatatagtttaaacctatgcacacagactacccttagtcttactgtgaagaattccagagg 361
Dbb 935 AAAATATAGTTAAACCATTTGCCACAGAAATCCCTCATATTTAGTGGAGAAATCCATTG 994
Qy 362 aaataacccgtgaatggaactgcttaagagccattccagcccaaaattttcatttatg 421
Dbb 995 ATATTAGATGAATGGAGCACACCTGGAGGACCCATTCACCAAGGTGTACACTTATG 1054
Qy 422 aaattgaattccacagagtgatgactacttgggtgactaccagcttgagaatgagatc 481
Dbb 1055 AAAATTTGTATCGGAGAACGACGATATTTCTGGGAGTCTGCCACAGACAAAACGATATGA 1114
Qy 482 aaatcacagaacatcaaatgaaagcccaaaatattgcttttggtaagaagtaagtg 541
Dbb 1115 AGTTGAAGGAGGACGAAATGAAGTGAAGACCTATGCTTTTGTAGATGTAAGGTCA 1174
Qy 542 atattattgctcagatgatggaactcctggagtgagtgagtgatgaacaatgctggaag 601
Dbb 1175 ATATATATTGTGACATGATGCAATTTGGAGCGAATGGAGTGAAGAGGAATGTTGGAAG 1234
Qy 602 gtgacatatggaaggaaccccttagtatttttttctgataccatttctgtctcaatat 561
Dbb 1235 GTTACACAGGGCCGAGCTCAAAAGATATTTTTCATAGTACCAGTTTGTCTTTTATAT 1294
Qy 662 ttgttttgtaataacttgcctgcttggatataagcaaggcttttactgaaacagatct 721
Dbb 1295 TCTTTTGTACTTCTTTGCCCTTTATTTGGAGAGGAACTGAACCCACATTTGAGCC 1354
Qy 722 ttc-----atacaaaaaaagagtccttttctcacaagacacattctgttgactcagta 775
Dbb 1355 TCCATGTGGATCTGAACAAAGAGTGTGCTTATGAAGATACCCTCTGTTTAAACCA 1414
Qy 776 actttcagctcttatggcgaatggttaaatatgatttattaaactgaagcttttctc 835
Dbb 1415 ATTTCTTGACATAGAGCCAG----CCAGCAGGAGTTCATATTAACCTCAA-TTTTCTCTTAA 1469
Qy 836 aaatattgaataactcttatttttaaaangaaaaa 878
Dbb 1470 AATTTCGAATACATCTTCTTGAATATCCAAAAA 1512

RESULT 7

US-08-846-340-1
; Sequence 1, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:

APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,340
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1525 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1404
US-08-846-340-1

Query Match 50.8%; Score 446; DB 4; Length 1525;
Best Local Similarity 71.5%; Pred. No. 6.3e-104;
Matches 631; Conservative 0; Mismatches 241; Indels 11; Gaps 3;

Qy 2 aaggaatcgggaactaaattcaagatatgagctggtgtatattacaaactggcaatt 61
Dbb 635 AAGGAAGTTTGGAACTAAATTCAGGACATGAAGTGATATATATTAACGGCAGTATT 694
Qy 62 tagtctgctctggaaactggcctggtgtccattttgataccaaactaccagttgttt 121
Dbb 695 TGGTCTGCTCTTGGAACTGCGAAGACAGATATATCTGTATACCAACTATACCATGTTTT 754
Qy 122 actggtatgagggctggaccattcagcagagtgctactgattacatcaagggttaattgaa 181
Dbb 755 TCTGGTATGAGGGCTTGGATCATGCTTACAGTGTGCTGATTTACCTCCAGCATGATGAAA 814
Qy 182 aaaaatgggagtcaggggttccctatttggagtcacagactataaagattttcacatct 241
Dbb 815 AAAATGTTGGATGCAAACTGTCCAATGGACTTCAGACTATAAAGATTTTTTATCT 874
Qy 242 gttttaaattgggtcatcagaatcccagccctatcagaccagctatttttttcagcttc 301
Dbb 875 GTGTTAAATGGATCTTCAAAGTTTGGAACTGAGATCCAGATCCAGCTATACAGTTTTTCAACTTC 934
Qy 302 aaatatagtttaaacctatgcacacagactacccttagtcttactgtgaagaattccagagg 361

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Db 935 AAAATATAGTAAACCATTCGCCACAGAAATTCCTTCATATTAGTGGAGAATTCATTTG 994
Qy 362 aaattaacatgaatggaacatgcctaaagaccatccagccaaatgcttcattatg 421
Db 995 ATATTAGATGAATGGAGCACACCTGGAGGACCATTCACCAAGGTGTACACTTATG 1054
Qy 422 aaattgaattcacagagatggtactactctgggtgactaccacacattgagaatgagatc 481
Db 1055 AAATTTGTGTCGAGAACGATATTTCTGGGAGCTGCCACACACAAAAACGATATGA 1114
Qy 482 aaatcacagaacatcaaatgaaacccaaataattatgcttttttgtaagaagtaagtga 541
Db 1115 AGTTGAAGAGGAGAGCAAAATGAAGTGAAGACCTATGTCTTTTGTAAAGATGAAGGTCA 1174
Qy 542 atattattgctcagatgatgaatctgagtgagtgagtgatgaacaatctggaag 601
Db 1175 ATATATATTGTCAGATGATGGAATTTGGAGCGAATGGAGTGAAGAGGAATTTGGGAG 1234
Qy 602 gtgacatatggaagaaacacattagtttttttattgataccatttgccttttctcaatat 661
Db 1235 GTTACACAGGGCCAGACTCAAGAGATTAATTTTCATAGTACCAGTTGTCTTTTATATAT 1294
Qy 662 ttgttttgtaataactgctgctgttttgataaagcaaaaggccttactgaaacgatct 721
Db 1295 TCCTTTGTACTTCTTTGCTTATTTGGAGTGAAGAAACCTCAACCCACATTTGAGGCC 1354
Qy 722 ttc-----atacaaaaaaagaagcttttctcatcaagacacatctgttgactcagta 775
Db 1355 TCCATGTGGATCTGAACAAAGAGTGTGTGTTATGAGATACCTCTGTAAACACCA 1414
Qy 776 acttcagctcttatggccagatgttaaatatgagctcttattaaactgaagcttttctccta 835
Db 1415 ATTTCTTGACATAGAGCCAG-----CCAGCAGGAGTCATATTAACTCAA-TTTCCTTAA 1469
Qy 836 aaattgtaataaactttattttaaangaaaaaataaaaaa 878
Db 1470 AATTTCGAATACATCTCTTGTGAAATTCCAAAAAAATAAAAAA 1512
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RESULT 8

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US-08-846-344-1
: Sequence 1, Application US/08846344
: Patent No. 6268480
: GENERAL INFORMATION:
: APPLICANT: Collins, Mary
: APPLICANT: Donaldson, Debra
: APPLICANT: Fitz, Lori
: APPLICANT: Neben, Tamlyn
: APPLICANT: Whitters, Matthew
: APPLICANT: Wood, Clive
: TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESS: Genetics Institute, Inc.
: STREET: 87 CambridgePark Drive
: CITY: Cambridge
: STATE: MA
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/846.344
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/609,572
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
```

```
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: REFERENCE/DOCKET NUMBER: G15268
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1525 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: HYPOTHETICAL: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 256..1404
: US-08-846-344-1

Query Match 50.8%; Score 446; DB 4; Length 1525;
Best Local Similarity 71.5%; Pred. No. 6.3e-104;
Matches 631; Conservative 0; Mismatches 241; Indels 11; Gaps 3;

Qy 2 aaggaaatcggaagaaactaaatcaagatatggaactgtgtatattacaactggcaatatt 61
Db 635 AAGGAAGTTTGGAAACTAAATTCAGGACATGAAGTGTATATATTATAACTGGCAGTATT 694
Qy 62 tagctgctcttggaactcgcatgggtgccattttgataccaattaccagttgtttt 121
Db 695 TGGTCTGCTCTTGGAAACCTGGCAAGACAGTATATTCTGATACCAACTATACCATGTTTT 754
Qy 122 actggtatgagggcttgaccattcagcagagtgactgactacatcaagggttaaaggaa 181
Db 755 TCTGTATGAGGGCTTGGATCATGCTTACAGTGTCTGCTATACCTCCAGCATGATGAA 814
Qy 182 aaaaatggatgcagggttccctatttggagtcacacagactataaagattctcaatct 241
Db 815 AAAATGTTGGATGCAAACTGTCCAACTTGGACTCATCAGACTATAAAGATTTTATATCT 874
Qy 242 gtgtaaatgggtcatcagaatcccagcctatcagaccagctatttttttcaagcttc 301
Db 875 GTGTTAATGGATCTTCAAAGTTGGAACCCATCAGATCCAGCTATACAGTTTTCACATTC 934
Qy 302 aaaaatagttaaacctatgccaccagacactaccttagtcttactgtgaagaattccagag 361
Db 935 AAAATATAGTTAAACCATTCGCCACAGAAATTCCTTCATATTAGTGGAGAAATTCATTTG 994
Qy 362 aaattaacatgaatggaacatgcctaaaggaccacattccagccaaatgcttcattatg 421
Db 995 ATATTAGAATGAATGGAGCACACCTGGAGGACCCATTCACCAAGGTGTACACTTATG 1054
Qy 422 aaattgaattcacagagatggtactacttgggtgactaccacacagttgagaatgagatc 481
Db 1055 AAATTTGTATCCGAGAAGACGATATTTCTGGGAGTCTGCCACAGACAAAAACGATATGA 1114
Qy 482 aaatcacagaacatcaaatgaaacccaaataattatgcttttttgtaagaagtaagtga 541
Db 1115 AGTTGAAGAGGAGAGCAAAATGAAGTGAAGACCTATGCTTTTGTAAAGATGAAGGTCA 1174
Qy 542 atattattgctcagatgatggaatctggagtgagtgagtgatgaacaatctggaag 601
Db 1175 ATATATATTGTCAGATGATGGAATTTGGAGCGAATGGAGTGAAGAGGAATTTGGGAG 1234
Qy 602 gtgacatatggaagaaacacattagtttttttattgataccatttgccttttctcaatat 661
Db 1235 GTTACACAGGGCCAGACTCAAAAGATTAATTTTCATAGTACCAGTTGTCTTTTATATAT 1294
Qy 662 ttgttttgtaataactgctgctgttttgataaagcaaaaggccttactgaaacgatct 721
Db 1295 TCCTTTGTACTTCTTTGCTTATTTGGAGTGAAGAAACCTCAACCCACATTTGAGGCC 1354
Qy 722 ttc-----atacaaaaaaagaagcttttctcatcaagacacattctgttgactcagta 775
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Db 1355 TCCATGTGGATCGAACAAAGGTGTGCTTATGAAGATACCCCTGTGTTAAACACCA 1414
      || | || | || | || | || | || | || | || | || | || | || | || |
Qy 776 accttcagcttattgagcagatgtaataatgagcttattataaactgaagcttttcctca 835
      || | || | || | || | || | || | || | || | || | || | || | || |
Db 1415 APTTCTTGACATGAGCAG-----CCAGCAGAGTCAATATTAAACTCAA-TTTCCTCTTAA 1469
      || | || | || | || | || | || | || | || | || | || | || | || |
Qy 836 aatattgaaataattctatttttaaaangaaaaaataaaaaa 878
      || | || | || | || | || | || | || | || | || | || | || | || |
Db 1470 AATTTCGAATACATCTTCTTGAAATCCAAAAAATAAAAAA 1512
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RESULT 9
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/232.463
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14
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Query Match 4.8%; Score 42.2; DB 1; Length 7218;
Best Local Similarity 2.7%; Pred. No. 0.12;
Matches 8; Conservative 171; Mismatches 114; Indels 0; Gaps 0;

Qy 327 agactacccttactgtaagaattccagaggaaattacctgaaatggaacatgcc 386
      || | || | : : : : : : : : : : : : : : : : : : : : : :
Db 1449 AGAACAATTGTGACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1390
      || | || | : : : : : : : : : : : : : : : : : : : : : :
Qy 387 taaaggaccattccagccaatgttctattatgaaattcacagaggatggtac 446
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1389 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1330
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Qy 447 tacttggtgactaccagttgagaatgagatcacaaatcacagaacacatcaaatgaaag 506
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1329 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1270
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 507 ccaaaaattatgcttttggtaagaagtaaaagtgaaattatttctcagatgatggaat 566
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1269 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1210
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 567 ctggagtgagtgagtgatgaaacaatgctggaagagtgacatatggaaggaaa 619
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1209 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1157

RESULT 10
US-08-261-663A-1
; Sequence 1, Application US/08261663A
; Patent No. 5571706
; GENERAL INFORMATION:
; APPLICANT: Baker, Barbara J
; APPLICANT: Whitham, Steven A
; TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Margaret A. Connor, USDA-ARS
; STREET: 800 Buchanan Street
; CITY: Albany
; STATE: CA
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261.663A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Connor, Margaret A
; REGISTRATION NUMBER: 30043
; REFERENCE/DOCKET NUMBER: 0094.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 559-6067
; TELEFAX: (510) 559-5777
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana glutinosa
; TISSUE TYPE: leaf
; FEATURE:
; NAME/KEY: exon
; LOCATION: join(294..772, 1003..2098, 2941..3213, 5032..6600,
; LOCATION: 6934..6951)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 773..1002
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2099..2940
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3214..5031
; FEATURE:
; NAME/KEY: intron
; LOCATION: 6601..6933
; FEATURE:
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```
; NAME/KEY: CDS
; LOCATION: join(294..772, 1003..2098, 2941..3213, 5032..6600,
; LOCATION: 6934..6951)
US-08-261-663A-1

Query Match      4.6%; Score 40; DB 1; Length 7400;
Best Local Similarity 43.9%; Pred. No. 0.42;
Matches 172; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

Qy 333 ccttagcttactgtgaagattcagaggaaattacacctgaaatggaacatgcctaaagg 392
Db 2395 CCAATGCTCTTCTTGGATTAACTTGAATAATTTATGACATTATATAATAACTCAATC 2454
Qy 393 accattccagccaaatgtttcattatgaattgaattcacagaggatggtactacttg 452
Db 2455 ATTCATTACCTTTACCATTTATTTTATATAAGTTACAATTTATTGCTACTGTTTC 2514
Qy 453 ggtgactaccacagttgagaatgagatgagatacaaatcacagaacatcaaatgaaagccaaaa 512
Db 2515 AGTTACAATTACTTCCCAACATGGAAACTTATAAAGTGGACTCCAATAAACTTATAAGA 2574
Qy 513 attatgcttttggtaagaagtaaaatgaaattatttattgctcagatgatggaactctggag 572
Db 2575 AAAATGTAATAATAGAAAATAAAATTTATATAATTAATAAATAAGTATTTTCTGAAG 2634
Qy 573 tgagtggagtgatgaacaatgctggaagggtgacataatggaaggaaaccttagtattttt 632
Db 2635 TAACATCAGTATTTCTTAAAGAAATCCAATTAACATTTGATCTTAAACTTTGGTATGCT 2694
Qy 633 ctgtataccatttgccttttgcctcaatatttgccttttgccttaactgcctgcttttga 692
Db 2695 AAGCGTGCAGAAAGTAGTGGCCTTATTTCAATTTGACGTGAAGATAGAAATGCCCTTTAA 2754
Qy 693 taagcaaaaggccttactgaaacagatctttc 724
Db 2755 CGACATAAGGGGAAGGGGCAAGAATAAGTTTC 2786

RESULT 11
PCT-US95-07754A-1
; Sequence 1, Application PC/TUS9507754A
; GENERAL INFORMATION:
; APPLICANT: Baker, Barbara J
; APPLICANT: Whitham, Steven A
; TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Margaret A. Connor, USDA-ARS
; STREET: 800 Buchanan Street
; CITY: Albany
; STATE: CA
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07754A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connor, Margaret A
; REGISTRATION NUMBER: 30043
; REFERENCE/DOCKET NUMBER: 0094.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 559-6067
; TELEFAX: (510) 559-5777
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7400 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana glutinosa
; TISSUE TYPE: leaf
; FEATURE:
; NAME/KEY: exon
; LOCATION: join(294..772, 1003..2098, 2941..3213, 5032..6600,
; LOCATION: 6934..6951)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 773..1002
; NAME/KEY: intron
; LOCATION: 2099..2940
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3214..5031
; FEATURE:
; NAME/KEY: intron
; LOCATION: 6601..6933
; NAME/KEY: CDS
; LOCATION: join(294..772, 1003..2098, 2941..3213, 5032..6600,
; LOCATION: 6934..6951)
PCT-US95-07754A-1
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Query Match 4.6%; Score 40; DB 5; Length 7400;
Best Local Similarity 43.9%; Pred. No. 0.42;
Matches 172; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

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Qy 333 ccttagcttactgtgaagattcagaggaaattacacctgaaatggaacatgcctaaagg 392
Db 2395 CCAATGCTCTTCTTGGATTAACTTGAATAATTTATGACATTATATAATAACTCAATC 2454
Qy 393 accattccagccaaatgtttcattatgaattgaattcacagaggatggtactacttg 452
Db 2455 ATTCATTACCTTTACCATTTATTTTATATAAGTTACAATTTATTGCTACTGTTTC 2514
Qy 453 ggtgactaccacagttgagaatgagatgagatacaaatcacagaacatcaaatgaaagccaaaa 512
Db 2515 AGTTACAATTACTTCCCAACATGGAAACTTATAAAGTGGACTCCAATAAACTTATAAGA 2574
Qy 513 attatgcttttggtaagaagtaaaatgaaattatttattgctcagatgatggaactctggag 572
Db 2575 AAAATGTAATAATAGAAAATAAAATTTATATAATTAATAAATAAGTATTTTCTGAAG 2634
Qy 573 tgagtggagtgatgaacaatgctggaagggtgacataatggaaggaaaccttagtattttt 632
Db 2635 TAACATCAGTATTTCTTAAAGAAATCCAATTAACATTTGATCTTAAACTTTGGTATGCT 2694
Qy 633 ctgtataccatttgccttttgcctcaatatttgccttttgccttaactgcctgcttttga 692
Db 2695 AAGCGTGCAGAAAGTAGTGGCCTTATTTCAATTTGACGTGAAGATAGAAATGCCCTTTAA 2754
Qy 693 taagcaaaaggccttactgaaacagatctttc 724
Db 2755 CGACATAAGGGGAAGGGGCAAGAATAAGTTTC 2786
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RESULT 12
US-08-451-405A-2/c
; Sequence 2, Application US/08451405A
; Patent No. 5736358
; GENERAL INFORMATION:
; APPLICANT: FASEL, NICOLAS JOSEPH
; APPLICANT: REYMOND, CHRISTOPHE DOMINIQUE
; TITLE OF INVENTION: DICTYOSTELID EXPRESSION VECTOR AND
; TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE WEBB LAW FIRM
; STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
; CITY: PITTSBURGH
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 15219-1818
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK
; COMPUTER: Midwest Micro 486-50
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451.405A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,273
; FILING DATE: 15-JAN-1993
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 731
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN
US-08-451-405A-2

Query Match 4.4%; Score 38.4; DB 1; Length 731;
Best Local Similarity 47.0%; Pred. No. 0.51;
Matches 117; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 630 ttcttgataccattgtttgtctcaatattttttgttgtaataactgcctctttt 689
Db 729 TTTTITTTAAATGTTGTTTITTAATGTTTITTTTAAAAAATAAAATTTT 670

QY 690 gtaagcaagggcttttactgaacacgatcttttcatacaaaaaaagaagtccttcca 749
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QY 750 tcaagacacattctgtgactcagtaactttcagctcttatggccagatgttaaatagag 809
Db 609 AAAGAAATATTATTACTACTATTAGGAAAAATATTTTCTAATGATATATATAA 550

QY 810 tcttataaactgaagcttttctcacaatatgataaactttttaaangaaaaa 869
Db 549 ATAAATAATAATAATGTTATTGTTGATTAAAGGGGTTGATGCTAAAAAATAA 490

QY 870 aaaaaaaa 878
Db 489 AAATTAATAA 481

RESULT 13
US-08-933-821-3
; Sequence 3, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933.821
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3355 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-933-821-3

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Best Local Similarity 49.7%; Pred. No. 0.82;
Matches 96; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 686 ttgtataagcaagggcttttactgaacacgatcttttcatacaaaaaaagaagtcctttt 745
Db 2360 TTAGGGAGAACTTCTAGTTTGGCAATAGAAAAATGTTCTCCATTGAATAAAGTTATT 2419

QY 746 ctcatcaagacacattctgtgactcagtaactttcagctcttatggccagatgttaataa 805
Db 2420 TCAAAATTGAATTTGTGCGCTTTCACACGTAATGATTAAATCTGAATTCCTTAATAATATATC 2479

QY 806 tgaagcttattaaactgaagcttttccctcaaatattgataaactttttttaaangaa 865
Db 2480 CTATGCTGATTTTCCCAAAACATGACCCCATAGTATTAAATACATATCATCTTTTAAAAATA 2539

QY 866 aaaaaaaa 878
Db 2540 AAAAAAACCCAA 2552

RESULT 14
US-08-960-507-3
; Sequence 3, Application US/08960507
; Patent No. 6057435
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960.507
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130p1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:13:30 ; Search time 559.18 Seconds
(without alignments)
2695.824 Million cell updates/sec

Title: US-09-828-995B-57
Perfect score: 878
Sequence: 1 caaggaatcgggaactaa.....aaangaaaaaaaaaaaaa 878

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	877	99.9	878	22	AA559960 Canine interleukin
c 2	877	99.9	878	22	AA559961 Canine interleukin
3	877	99.9	1454	22	AA559962 Canine interleukin
c 4	877	99.9	1454	22	AA559963 Canine interleukin
5	765	87.1	1095	22	AA559966 Canine interleukin
c 6	765	87.1	1095	22	AA559967 Canine interleukin
7	765	87.1	1158	22	AA559964 Canine interleukin
c 8	765	87.1	1158	22	AA559965 Canine interleukin
9	617.8	70.4	954	22	AA559968 Canine IL-13R extr

c 10	617.8	70.4	954	22	AA559969 Canine IL-13R extr
11	617.8	70.4	1686	22	AA559970 Canine IL-13R/IgG-
c 12	617.8	70.4	1686	22	AA559971 Canine IL-13Ralpha
13	617.8	70.4	1686	22	AA559976 Canine IL-13R/IgG-
c 14	617.8	70.4	1686	22	AA559977 Canine IL-13Ralpha
15	617.8	70.4	1692	22	AA559974 Canine IL-13R/IgG-
c 16	617.8	70.4	1692	22	AA559975 Canine IL-13Ralpha
17	617.8	70.4	1698	22	AA559972 Canine IL-13R/IgG-
c 18	617.8	70.4	1698	22	AA559973 Canine IL-13Ralpha
19	534	60.8	1298	18	AA559974 Human interleukin-
20	534	60.8	1298	22	AA559975 Nucleotide sequenc
21	533.6	60.8	1288	19	AA559976 Human HR-1 recepto
22	533.6	60.8	1288	19	AA559977 Human cytokine/pep
23	533.6	60.8	1288	19	AA559978 Homo sapiens cDNA
24	533.6	60.8	1369	18	AA559979 cDNA encoding the
25	533.6	60.8	1369	21	AA559980 cDNA encoding IL-1
26	533.6	60.8	1369	22	AA559981 Human interleukin-
c 27	533.6	60.8	1369	22	AA559982 Human interleukin-
28	533.6	60.8	1369	22	AA559983 Human IL-13 recept
29	533.6	60.4	1289	18	AA559984 Human zcytor2 cyto
30	530.6	60.4	1289	18	AA559985 Human zcytor2 cyto
31	497.6	56.7	1126	18	AA559986 Celebus macaque 2c
32	493.2	56.2	1167	18	AA559987 Human zcytor2 cyto
33	451.6	51.4	947	19	AA559988 Mature interleukin
34	451.6	51.4	1079	19	AA559989 Construct containi
35	451.4	51.4	951	24	AA559990 Human soluble cyto
36	446	50.8	1525	18	AA559991 cDNA encoding the
37	446	50.8	1525	21	AA559992 cDNA encoding IL-1
38	446	50.8	1525	22	AA559993 Mouse interleukin-
c 39	446	50.8	1525	22	AA559994 Mouse interleukin-
40	446	50.8	1525	22	AA559995 Murine interleukin
41	446	50.8	1525	22	AA559996 Mouse IL-13 recept
42	246	28.0	1539	18	AA559997 Human interleukin-
43	150.4	17.1	465	19	AA559998 Interleukin-13 bin
44	49.6	5.6	38342	22	AA559999 Tumour suppressor
c 45	46.2	5.3	18598	24	AA559998 Human immune syste

ALIGNMENTS

RESULT 1

AA559960

ID AA559960 standard; cDNA; 878 BP.

XX AC AA559960;

XX AC AA559960;

DT 29-JAN-2002 (first entry)

XX Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 878.

DE Canine interleukin 13 receptor alpha1; interleukin-13 receptor alpha2;

XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;

KW IL-13Ralpha; IL-13Ralpha2; immunoglobulin heavy chain; IgG Fc;

KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;

XX immune response.

XX Canis familiaris.

OS Canis familiaris.

XX WO200177332-A2.

PN WO200177332-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001WO-US11498.

PF 07-APR-2000; 2000US-195659P.

XX 07-APR-2000; 2000US-195874P.

PR (HESK-) HESKA CORP.

PA McCall CA, Tang L;

XX WPI; 2001-657172/75.

XX P-PSDB; AAU69134.

DR

XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
PS
XX Claim 19; Page 170-171; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13 proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13alpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13 mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
SQ Sequence 878 BP; 298 A; 141 C; 165 G; 273 T; 1 other;

Query Match 99.9%; Score 877; DB 22; Length 878;
Best Local Similarity 100.0%; Pred. No. 9.6e-193;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 caaggaatcgggaactaaattcaagatgactgtgactgtgtattatacaactggcaatat 60
DB 1 caaggaatcgggaactaaattcaagatgactgtgactgtgtattatacaactggcaatat 60
QY 61 ttactgtctcttggaacctggatgggtgtccattttgtatatacaattaccagttgttt 120
DB 61 ttactgtctcttggaacctggatgggtgtccattttgtatatacaattaccagttgttt 120
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DB 121 tactgtgtatgagggttgaccattcagcagagtgtactgtattacataaggttaattga 180
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DB 181 aaaaatatggatgcaggtttccctatttgagtcatacagactataaagattttacatat 240
QY 241 tgtgttaattggttcacatcagaatccagcttatcagaccagctatttttttcagctt 300
DB 241 tgtgttaattggttcacatcagaatccagcttatcagaccagctatttttttcagctt 300
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DB 301 caaaatatagttaaacctatgccaccagactaccttagtcttactgtgaagaattcagag 360
QY 361 gaaattaaacctgaaatgaaacatgctaaaggaccattccagcacaattgtttcatttat 420
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QY 421 gaaattgaaatcacagagatggttactacttgggtgactacacagttgagaatgagata 480
DB 421 gaaattgaaatcacagagatggttactacttgggtgactacacagttgagaatgagata 480
QY 481 caaatcaagaacatcaaatgaaagccaaaattatgtcttttggtaagagtaaatgtg 540
DB 481 caaatcaagaacatcaaatgaaagccaaaattatgtcttttggtaagagtaaatgtg 540
QY 541 aatatatttgcctcagatgatggaatcctggagtgagtgagtgatgaaacatgctggaaa 600
DB 541 aatatatttgcctcagatgatggaatcctggagtgagtgagtgatgaaacatgctggaaa 600
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Db 661 tttgttttggttaataacttgctgtctttgtataagcaagggttttactgaaaacgatac 720
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QY 841 tgaataatcttatttttaaaangaaaaaataaaaaaa 878
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RESULT 2
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ID AAS59961 standard; cDNA; 878 BP.
XX
AC AAS59961;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 878 complement.
XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI; 2001-657172/75.
XX

Novel isolated canine protein, preferably canine immunoglobulin G protein or canine interleukin-13 receptor protein useful for regulating immune response of an animal and for developing regulatory compounds -

Claim 19; Page 172-173; 221pp; English.

The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13 proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13alpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13 mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence is the reverse complement of a cDNA encoding a protein of the invention.

SQ Sequence 878 BP; 273 A; 165 C; 141 G; 298 T; 1 other;

Query Match 99.9%; Score 877; DB 22; Length 878;

Db 877 caaaatagttataaacctatgccaccagactacotttagttcttactgtgaagaattcaag 936
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Db 937 gaaataacccgaaatggaacatgctaaaggaccattccagccaaatgtttctattat 996
Qy 421 gaaattgaattcacagagatggtactactctgggtgaactaccacagttgaaatgagata 480
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Qy 601 ggtgacatatggaagaaacotttagtatttttttcttgataaccattgctttgtctcaata 660
Db 1177 ggtgacatatggaagaaacotttagtatttttttcttgataaccattgctttgtctcaata 1236
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Db 1237 ttgttttggtaataactgctgctgttttataagcaaaaggcctttactgaaacgcatc 1296
Qy 721 ttctacacaaaaaagaagttctttctcatcaagacacattctgttgactcagtaacctt 780
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Db 1357 cagtccttatggccagatgttaaatatgatttatttaaaactgaagccttttctcacaatat 1416
Qy 841 tgaataaatcttatttttaaaangaaaaaataaaaaa 878
Db 1417 tgaataaatcttatttttaaaangaaaaaataaaaaa 1454

RESULT 4
AAS59963/C
ID AAS59963 standard; cDNA; 1454 BP.
XX
AC AAS59963;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1454 complement.
XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
XX WO200177332-A2.
PN
XX
PD 18-OCT-2001.
XX
XX
PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
XX (HESK-) HESKA CORP.
XX
XX McCall CA, Tang L;
PI
XX
DR WPI; 2001-657172/75.
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating

immune response of an animal and for developing regulatory compounds -
Claim 19; Page 177-178; 221pp; English.
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX
SQ Sequence 1454 BP; 442 A; 282 C; 238 G; 491 T; 1 other;

Query Match 99.9%; Score 877; DB 22; Length 1454;
Best Local Similarity 100.0%; Pred. No. 1.1e-192;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 878 CAAGAAATCGGAAACTAAAATTCAAGATATGGACTGTGTATATTACAACCTGGCAATAT 819
Qy 61 ttactgtctcttggaaacctgggaatgggtgtccattttgtatatacaactacagttgttt 120
Db 818 TTACTGTCTCTTGGAAACCTGGCATGGGTGTCCATTTTGTATACCAATTACCAAGTTGTTT 759
Qy 121 tactgtgtatgaggccttgaccattcagcagtgactgtactgattacatcaaggttaattga 180
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Qy 241 tgtgttaatgggtcacaagaatccagcctatcagacccagcctattttttttcagctt 300
Db 638 TGTGTTAATGGGTGCATCAGAATCCAGCTATCAGACCAGCTATTTTATTATTTTTCAGCTT 579
Qy 301 caaaatagttataaacctatgccaccagactaccttagtcttactgtgaagaattcagag 360
Db 578 CAAAATATAGTTAAACCTATGCCACCAGACTACCTTAGTCTTACTGTGAAGAAATTCAGAG 519
Qy 361 gaaatcaacctgaaatggaacatgcctaaaggaccattccagccaaatgtttctattat 420
Db 518 GAAATTAACCTGAAATGGAACATGCCTAAAGGACCCATTCACGCCAAATGTTTCATTAT 459
Qy 421 gaaattgaattcacagagatgggtactactctgggtgaactaccacagttgaaatgagata 480
Db 458 GAAATTTGAATTCACAGAGGATGGTACTACTTGGGTGAGTACCACAGTTGAGAATGAGATA 399
Qy 481 caaatcacagaacatcaaatgaaaggccaaataattatgcttttggtaagaagtaaaagt 540
Db 398 CAAATCACAGAACATCAAAATGAAAGCCAAAATATATGCTTTTGGTAAGAAATGTAAGTG 339
Qy 541 aatatttattgctcagatgatggaatcgtggagtgagtgagtgatgaacaatgctggaaa 600
Db 338 AATATTTATTGCTCAGATGATGGAATCTGGAGTGGAGTGAGTGATGAACAATGCTGGAAA 279
Qy 601 ggtgacatatggaagaaacotttagtatttttcttgataaccattgctttgtctcaata 660
Db 278 GGTGACATATGGAAGAAACCTTAGTATTTTCTTGATACCAATTTGCTTTTGTCTCAATA 219
Qy 661 ttgttttggtaataactgctgctgttttataagcaaaaggcctttactgaaacgcatc 720
Db 218 TTTGTTTGGTAATAACTTGCTTGTCTTTTGTATAAAGAAAGGGCTTTACTGAAACGATC 159

```
QY 721 tttcatcaaaaaaagaagcttttttctcatcaagaacacattctgttgaactcagtaacttt 780
D 158 TTTTCATACAAAAAAGAGTCTTTTCTCATCAAGACACATTCTCTTGACTCAGTAACTTT 99
QY 781 cagctcttatgcccagatgttaaatatagctcttattaaactgaagcttttccctcaaatat 840
D 98 CAGTCTTATGCCACAGATGTTAAATATGAGTCTTATTAACTGAAGACTTTTCTCCTCAATAT 39
QY 841 tgaataaactcttattttaaaangaaaaaataaaaaa 878
D 38 TGAATAAATCTTATTTTAAANGAAAAAATAAAAAA 1

RESULT 5
AAS59966
ID AAS59966 standard; cDNA; 1095 BP.
AC AAS59966;
XX
XX
XX 29-JAN-2002 (first entry)
DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1095.
XX
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
XX Canis familiaris.
OS
XX
XX WO200177332-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 09-APR-2001; 2001WO-US11498.
XX
XX 07-APR-2000; 2000US-195659P.
PR
XX 07-APR-2000; 2000US-195874P.
XX
XX (HESK-) HESKA CORP.
PA
XX
XX McCall CA, Tang L;
PI
XX
XX WIPI; 2001-657172/75.
DR
XX P-PSDB; AAU69136.
DR
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds.
XX
XX Claim 19; Page 179-181; 221pp; English.
XX
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
XX Sequence 1095 BP; 370 A; 186 C; 211 G; 328 T; 0 other;
SQ

Query Match 87.1%; Score 765; DB 22; Length 1095;
Best Local Similarity 100.0%; Pred. No. 6.3e-167;
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 caaggaatcgggaaactaaatcaagatatggactgtgtattattacaactggcaatat 60
D 331 caaggaatcgggaaactaaatcaagatatggactgtgtattattacaactggcaatat 390
QY 61 ttaagtcgtctcttgaaacacctggcatgggtgtccatttttgataccaattaccagttggtt 120
D 391 ttagtcgtctcttgaaacacctggcatgggtgtccatttttgataccaattaccagttggtt 450
QY 121 tactgggtatggggcttggaaccattcagcagagtgactgattacatcaaggttlaattgga 180
D 451 tactgggtatggggcttggaaccattcagcagagtgactgattacatcaaggttlaattgga 510
QY 181 aaaaatatgggatgcaggtttccctatttggagtcacacagactataaagattttcacatc 240
D 511 aaaaatatgggatgcaggtttccctatttggagtcacacagactataaagattttcacatc 570
QY 241 tgtgttaatgggtcatcagaatccagcagcctcatcagaccagcagctattttatttttcagctt 300
D 571 tgtgttaatgggtcatcagaatccagcagcctcatcagaccagcagctattttatttttcagctt 630
QY 301 caaaatatagttaaacctatgccaccagactacaccttagtcttactgtgaagaattccagag 360
D 631 caaaatatagttaaacctatgccaccagactacaccttagtcttactgtgaagaattccagag 690
QY 361 gaaattaacctgaaatggaacatgcctaaaggacccattccagccaaatgtttcatttat 420
D 691 gaaattaacctgaaatggaacatgcctaaaggacccattccagccaaatgtttcatttat 750
QY 421 gaaattgaattcacagaggtggtactacttgggtgactaccacagttgagaatgagata 480
D 751 gaaattgaattcacagaggtggtactacttgggtgactaccacagttgagaatgagata 810
QY 481 caaatcaagaacatcaaatgaaagccaaataattgcttttttggttaagaagtaaaagt 540
D 811 caaatcaagaacatcaaatgaaagccaaataattgcttttttggttaagaagtaaaagt 870
QY 541 aatatttattgctcagatgaggaatctggagtgagtgagtgagtgagtgagtgagtgagtgag 600
D 871 aatatttattgctcagatgaggaatctggagtgagtgagtgagtgagtgagtgagtgagtgag 930
QY 601 ggtgacatatggaaggaaaccttagtatttttcttgataccattgtgtttgtctcaata 660
D 931 ggtgacatatggaaggaaaccttagtatttttcttgataccattgtgtttgtctcaata 990
QY 661 ttgttttggttaataacttgcctcttttataagcaaaaggccttactgaaacagcatc 720
D 991 ttgttttggttaataacttgcctcttttataagcaaaaggccttactgaaacagcatc 1050
QY 721 tttcatcaaaaaaagaagcttttttctcatcaagaacacattctgt 765
D 1051 tttcatcaaaaaaagaagcttttttctcatcaagaacacattctgt 1095

RESULT 6
AAS59967/C
ID AAS59967 standard; cDNA; 1095 BP.
XX
XX AAS59967;
AC
XX
XX 29-JAN-2002 (first entry)
DT
XX
XX Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1095 complement.
DE
XX
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
XX Canis familiaris.
OS
XX
XX WO200177332-A2.
PN
XX
```

PD	18-OCT-2001.	
XX		
PF		
XX	09-APR-2001; 2001WO-US11498.	
PR	07-APR-2000; 2000US-195659P.	
PR	07-APR-2000; 2000US-195874P.	
XX		
PA	(HESK-) HESKA CORP.	
XX		
PI	McCall CA, Tang L;	
XX		
DR	WPI; 2001-657172/75.	
XX		
PT	Novel isolated canine protein, preferably canine immunoglobulin G	
PT	protein or canine interleukin-13 receptor protein useful for regulating	
PT	immune response of an animal and for developing regulatory compounds	
XX		
PS	Claim 19; Page 183; 221pp; English.	
XX		
CC	The invention concerns an isolated canine protein, preferably canine	
CC	immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)	
CC	receptor protein, the nucleic acids encoding them, antibodies	
CC	raised against them, fusion proteins between the IgG and IL-13R proteins	
CC	and methods of isolating regulators of them. The regulators are useful	
CC	for regulating an immune response in a canine. The proteins are useful to	
CC	develop regulatory compounds including inhibitors and activators that,	
CC	when administered to a canine in an effective manner, are capable of	
CC	protecting canine from disease mediated by IL-13Ralpha or IL-13. The	
CC	regulators are useful for treating canine IgG (heavy and/or light chain)	
CC	and/or canine IL-13R mediated responses. The molecules of the invention	
CC	are useful to regulate the immune response of an animal (e.g. by gene	
CC	therapy). The present sequence is the reverse complement of a cDNA	
XX	encoding a protein of the invention.	
XX		
SQ	Sequence 1095 BP; 328 A; 211 C; 186 G; 370 T; 0 other;	
Query Match 87.1%; Score 765; DB 22; Length 1095;		
Best Local Similarity 100.0%; Pred. No. 6.3e-167;		
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 caaggaatcgggaaactaaattcaagatatgactgactgtatattacaactggcaatat 60	
DB	765 CAAGGAAATCGGAAACCTAAATTCAGATATGGACTGTGTATATACAACTGGCAATAT 706	
QY	61 ttactgtctcttgaacctggcatgggtgtccattttgatccaataccagtgttt 120	
DB	705 TTAGTCTCTCTTGAAACCTGGCATGGGTGTCCATTTTGATACCAATTACCAAGTTGTTT 646	
QY	121 tactgtgatagggtcttgaccattcagcagagtgtactgattacatcaaggtttaattgga 180	
DB	645 TACTGGTATGAGGCTTGACCATTTCAGCAGAGTGTACTGATTACATCAAGGTTAATGGA 586	
QY	181 aaaaatacggatgcaggtttccctatttgagtcacagactacagactataagatttcacatc 240	
DB	585 AAAAATATGGATGTCAGGTTTCCCTATTGGAGTCATCAGACTATAAAGATTTCTACATC 526	
QY	241 tctgttaatgggtcatcagaatccagcctatcagaccagctatttttttcagttt 300	
DB	525 TGTGTTAATGGGTCTATCAGATGCCAGGCTATCAGACCCAGCTATTTTATTTCAGGTT 466	
QY	301 caaatacagtttaaacctatgcacacagactaccttagtcttactgtgaaagaattcagag 360	
DB	465 CAAATATAGTTAAACCTATGCCACCAGACTACCTTAGTCTTACTGTGAAGAAATTCACAG 406	
QY	361 gaaataacacctgaatggaacatgcctaaaggaccatccagcgaatgttttcattat 420	
DB	405 GAAATTAACCTGAAATGGAACATGCTCTAAAGACCCATTCACGCAAAATGTTTCATTTAT 346	
QY	421 gaaattgaattcacagagatggttactacttgggtgactaccacaggttgagaatagata 480	
DB	345 GAAATTAATTCACAGAGATGGTACTACTTGGGTGATCTACACACAGTTGAGAAATGAGATA 286	
QY	481 caaatcacagaacatcaaatgaaagccaaaattatgcttttttgtaagaagtaaatg 540	
DB	285 CAAATCACAGAACATCAATGAAGCCCAAAATTTATGCTTTTGGTAAAGAGTAAAGTG 226	
QY	541 aatattttgctcagatgatggaaatcctggagtgagtgagtgatgaacaaatgctggaaa 600	
DB	225 AATATTTTATGCTCAGATGATGGAATCTGGAGTGAAGTGAATGAACAATGCTGGAAA 166	
QY	601 ggtgacatgaaagaaaccttagtatttttcttgatcaccattgctttgtctcaata 660	
DB	165 GGTGACATATGAAGAAACCTTAGTATTTTCTTGATACCATTTGCTTTTGTCTCAATA 106	
QY	661 ttgttttggttaataactgctgctttgttataagcaaaaggctttactgaaaacgctc 720	
DB	105 TTTGTTTGGTAAATAACTTGCCTGCTTTTGTATAAGCAAGGGCTTTACTGAAAACGATC 46	
QY	721 ttctatacaaaaaagaagtgcttttctctcatcaagaacacattctgt 765	
DB	45 TTTTCATACAAAAAAGAGTCTTTTCTCATCAAGACACATTCTGT 1	
RESULT 7		
AAS59964		
ID	AAS59964 standard; cDNA; 1158 BP.	
AC	AAS59964;	
XX		
DT	29-JAN-2002 (first entry)	
DE	Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1158.	
XX		
KW	Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;	
KW	IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;	
KW	immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;	
KW	immune response.	
XX		
OS	Canis familiaris.	
PN	WO200177332-A2.	
XX		
PD	18-OCT-2001.	
XX		
PF	09-APR-2001; 2001WO-US11498.	
XX		
PR	07-APR-2000; 2000US-195659P.	
PR	07-APR-2000; 2000US-195874P.	
XX		
PA	(HESK-) HESKA CORP.	
XX		
PI	McCall CA, Tang L;	
XX		
DR	WPI; 2001-657172/75.	
XX		
PT	Novel isolated canine protein, preferably canine immunoglobulin G	
PT	protein or canine interleukin-13 receptor protein useful for regulating	
PT	immune response of an animal and for developing regulatory compounds	
XX		
PS	Claim 19; Page 178; 221pp; English.	
XX		
CC	The invention concerns an isolated canine protein, preferably canine	
CC	immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)	
CC	receptor protein, the nucleic acids encoding them, antibodies	
CC	raised against them, fusion proteins between the IgG and IL-13R proteins	
CC	and methods of isolating regulators of them. The regulators are useful	
CC	for regulating an immune response in a canine. The proteins are useful to	
CC	develop regulatory compounds including inhibitors and activators that,	
CC	when administered to a canine in an effective manner, are capable of	
CC	protecting canine from disease mediated by IL-13Ralpha or IL-13. The	
CC	regulators are useful for treating canine IgG (heavy and/or light chain)	
CC	and/or canine IL-13R mediated responses. The molecules of the invention	
CC	are useful to regulate the immune response of an animal (e.g. by gene	
CC	therapy). The present sequence is the reverse complement of a cDNA	
XX	encoding a protein of the invention.	
XX		

SQ Sequence 1158 BP; 380 A; 201 C; 224 G; 353 T; 0 other;

Query Match 87.1%; Score 765; DB 22; Length 1158;
Best Local Similarity 100.0%; Pred. No. 6.4e-167;
Matches 765; Conservative 0; Mismatches 0; Indels 0

Qy	1	caaggaatcgggaactaaaaatcaagatataggactgtgtataattacaactcggcaatat	60
Db	394	caaggaatcgggaactaaaaatcaagatataggactgtgtataattacaactcggcaatat	453
		caaggaatcgggaactaaaaatcaagatataggactgtgtataattacaactcggcaatat	453
Qy	61	ttagctcgtctcttgaaaacctggcattgggtgtccatttgataccaattaccagttgctt	120
Db	454	ttagctcgtctcttgaaaacctggcattgggtgtccatttgataccaattaccagttgctt	513
		ttagctcgtctcttgaaaacctggcattgggtgtccatttgataccaattaccagttgctt	513
Qy	121	tactggtatgagggcttggaaccttcagaccattcagcagagtgctactgattacaatcaaggttaatgga	180
Db	514	tactggtatgagggcttggaaccttcagaccattcagcagagtgctactgattacaatcaaggttaatgga	573
		tactggtatgagggcttggaaccttcagaccattcagcagagtgctactgattacaatcaaggttaatgga	573
Qy	181	aaaaatatgggatagcaggtttccctatttggagtcatacagactataaagatttctacatc	240
Db	574	aaaaatatgggatagcaggtttccctatttggagtcatacagactataaagatttctacatc	633
		aaaaatatgggatagcaggtttccctatttggagtcatacagactataaagatttctacatc	633
Qy	241	tgtgtaatgggttcatacagaatccagcctatcagaccagctattttatttttcagctt	300
Db	634	tgtgtaatgggttcatacagaatccagcctatcagaccagctattttatttttcagctt	693
		tgtgtaatgggttcatacagaatccagcctatcagaccagctattttatttttcagctt	693
Qy	301	caaaaatatgtttaaacctatgcaccagactaccttagtcttactgtgaagaatttcagag	360
Db	694	caaaaatatgtttaaacctatgcaccagactaccttagtcttactgtgaagaatttcagag	753
		caaaaatatgtttaaacctatgcaccagactaccttagtcttactgtgaagaatttcagag	753
Qy	361	gaaataaacctgaaatgggaacatgcctaaaggagcccaattccagcgaataatgtttcatttat	420
Db	754	gaaataaacctgaaatgggaacatgcctaaaggagcccaattccagcgaataatgtttcatttat	813
		gaaataaacctgaaatgggaacatgcctaaaggagcccaattccagcgaataatgtttcatttat	813
Qy	421	gaaatgaaattcacagaggaatgtactacttgggtgtaactcacacagttgagaatcagata	480
Db	814	gaaatgaaattcacagaggaatgtactacttgggtgtaactcacacagttgagaatcagata	873
		gaaatgaaattcacagaggaatgtactacttgggtgtaactcacacagttgagaatcagata	873
Qy	481	caaatcaagaagaacatacaaatgaaagccaaaataatgctttttggtagaagaagtaagtg	540
Db	874	caaatcaagaagaacatacaaatgaaagccaaaataatgctttttggtagaagaagtaagtg	933
		caaatcaagaagaacatacaaatgaaagccaaaataatgctttttggtagaagaagtaagtg	933
Qy	541	aataatttatgctcagatgatgaaatctcgagtgagtgagtgatgaacaaatcgtcggaaa	600
Db	934	aataatttatgctcagatgatgaaatctcgagtgagtgagtgatgaacaaatcgtcggaaa	993
		aataatttatgctcagatgatgaaatctcgagtgagtgagtgatgaacaaatcgtcggaaa	993
Qy	601	ggtgacataatggaaggaaaaccttagtattttcttgataccatttgccttttgcctcaata	660
Db	994	ggtgacataatggaaggaaaaccttagtattttcttgataccatttgccttttgcctcaata	1053
		ggtgacataatggaaggaaaaccttagtattttcttgataccatttgccttttgcctcaata	1053
Qy	661	ttgttttttggtaataacttgcctcgttttttgataaagcaaggcctttactgaaaaacgac	720
Db	1054	ttgttttttggtaataacttgcctcgttttttgataaagcaaggcctttactgaaaaacgac	1113
		ttgttttttggtaataacttgcctcgttttttgataaagcaaggcctttactgaaaaacgac	1113
Qy	721	tttcatcaaaaaaagaagtcttttttctcatcaagacacattctgt	765
Db	1114	tttcatcaaaaaaagaagtcttttttctcatcaagacacattctgt	1158
		tttcatcaaaaaaagaagtcttttttctcatcaagacacattctgt	1158

RESULT	8
AAS59965/c	
ID	AAS59965 standard; cDNA; 1158 BP.
XX	
XX	
AC	AAS59965;
XX	
DT	29-JAN-2002 (first entry)
XX	
DE	Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1158 complement.
XX	
KW	Dqg; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW	IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
KW	immunoglobulin light chain; lambda; ss; immunosuppressive gene therapy.

KW	immune response.
XX	
OS	Canis familiaris.
XX	
PN	WO200177332-A2.
XX	
PD	18-OCT-2001.
XX	
PF	09-APR-2001; 2001WO-US11498.
XX	
PR	07-APR-2000; 2000US-195659P.
PR	07-APR-2000; 2000US-195874P.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	McCall CA, Tang L;
XX	
DR	WPI; 2001-657172/75.
XX	
PT	Novel isolated canine protein, preferably canine immunoglobulin G
PT	protein or canine interleukin-13 receptor protein useful for regulating
PT	immune response of an animal and for developing regulatory compounds -
XX	
PS	Claim 19; Page 179; 221pp; English.
XX	
CC	The invention concerns an isolated canine protein, preferably canine
CC	immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC	receptor protein, the nucleic acids encoding them, antibodies
CC	raised against them, fusion proteins between the IgG and IL-13R proteins
CC	and methods of isolating regulators of them. The regulators are useful
CC	for regulating an immune response in a canine. The proteins are useful
CC	for regulating an immune response including inhibitors and activators that,
CC	when administered to a canine in an effective manner, are capable of
CC	protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC	regulators are useful for treating canine IgG (heavy and/or light chain)
CC	and/or canine IL-13R mediated responses. The molecules of the invention
CC	are useful to regulate the immune response of an animal (e.g. by gene
CC	therapy). The present sequence is the reverse complement of a cDNA
CC	encoding a protein of the invention.
XX	
SQ	Sequence 1158 BP; 353 A; 224 C; 201 G; 380 T; 0 other;
XX	

Query Match	87.1%	Score	765;	DB	22;	Length	1158;
Best Local Similarity	100.0%;	Pred.	No. 6,	4e-167;			
Matches	765;	Conservative	0;	Mismatches	0;	Indels	0; Gaps
Oy	1	caagaaatcggaacataaaaattcaagaatgactgatgactgtatatattacaactgcgaatat	60				
Dbb	765	CAAGAAATCGGAAACATAAATTCAAAGATGGACTGTGTATATTACAATTCGCNATAT	706				
Oy	61	ttagtctgctcttggaacctggcatgggtgccattttgtaccaatcaccagtgttt	120				
Dbb	705	TTAGTCTGCTCTTGGAACCTGGCATGGGTGCCATTTTGATACCATTACCAAGTTGTT	646				
Oy	121	tactggtataggggcttggaccaattccagcagtgctattcatcataagggttaattgga	180				
Dbb	645	TACTGGTATGAGGGCTTGACCAATTCAGCAGAGTCTACTGATTACATCAAGGTTAATGGA	586				
Oy	181	aaaaatataggatgcaggtttcccttatitggagtcatacagactataaagattttcacatc	240				
Dbb	585	AAAAATATGGATGCGAGGTTTTCCCTATTGTGGAGTCATCAGACTATAAGAATTTCTACATC	526				
Oy	241	tgtgttaatgggtcatcagaatcccagccctatcagaccacgtattttatttttcagctt	300				
Dbb	525	TGTGTTAATGGGTCAATCAGATCCAGGCTATCACACCAGCATATTTATTTTTCAGGTT	466				
Oy	301	caaaatatagtttaaaccctatgcaccagactacccttagtcttactgtgaagaattcagag	360				
Dbb	465	CAAAATATAGTTTAACCTATGCCACCACACTACCTTAGTCYTACTGTGAAAGNATTCAGAG	406				
Oy	361	gaaattaacctgaaatggaaatgcctcaaaaggaccattccagagccaatgttttcattat	420				


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Query Match          70.4%; Score 617.8; DB 22; Length 1686;
Best Local Similarity 99.7%; Pred. No. 5.7e-133;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caaggaaatcggaactaaattcaagatatggaactgtgtatatatacaactggcaaatat 60
Db 334 caaggaaatcggaactaaattcaagatatggaactgtgtatatatacaactggcaaatat 393

Qy 61 ttagtctctcttggaaacctgggaatgggtgtccattttgtatatacaaataccagttgttt 120
Db 394 ttagtctctcttggaaacctgggaatgggtgtccattttgtatatacaaataccagttgttt 453

Qy 121 tactgtgtatgagggttggacattcagcagagtgactgtactgtattacatcaagggttaattgga 180
Db 454 tactgtgtatgagggttggacattcagcagagtgactgtattacatcaagggttaattgga 513

Qy 181 aaaaataatggatgcaggtttccctattttgagtcacatcagactataaagattttcacatc 240
Db 514 aaaaataatggatgcaggtttccctattttgagtcacatcagactataaagattttcacatc 573

Qy 241 tgtgttaatgggttcacagaatccagcctatccagcctatccagcctatcttttttttccagctt 300
Db 574 tgtgttaatgggttcacagaatccagcctatccagcctatccagcctatcttttttttccagctt 633

Qy 301 caaaatatagttaaacctatgccaccagactacaccttagtcttactgtgaagaattccagag 360
Db 634 caaaatatagttaaacctatgccaccagactacaccttagtcttactgtgaagaattccagag 693

Qy 361 gaaataacctgaaatggaacatgcctcaaggaacccatccagcgaatgttttccatttat 420
Db 694 gaaataacctgaaatggaacatgcctcaaggaacccatccagcgaatgttttccatttat 753

Qy 421 gaaattgaattcacagagatggtactacttgggtgactacacagttgagaatgagata 480
Db 754 gaaattgaattcacagagatggtactacttgggtgactacacagttgagaatgagata 813

Qy 481 caaatccacaagaacatcaaatgaaaggccaaataattatgcttttggtaagaagtaaaagt 540
Db 814 caaatccacaagaacatcaaatgaaaggccaaataattatgcttttggtaagaagtaaaagt 873

Qy 541 aatatatttctgcagatgatggaatctgggaatctggagtgagtgatgaacaatgctggaaa 600
Db 874 aatatatttctgcagatgatggaatctgggaatctggagtgagtgatgaacaatgctggaaa 933

Qy 601 ggtgacatctggaaggaaacc 621
Db 934 ggtgacatctggaaggaaacc 954

RESULT 12
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ID AAS59971 standard; cDNA; 1686 BP.
XX
AC AAS59971;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine IL-13ralpha2/Ig-Fc fusion protein cDNA reverse complement.
DE
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13ralpha1; IR-13ralpha2; immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
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PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX (HESK-) HESKA CORP.
XX McCall CA, Tang L;
XX WPI; 2001-657172/75.
XX
PT Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX Example 4; Page 193-194; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ra1pha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX
SQ Sequence 1686 BP; 407 A; 382 C; 384 G; 513 T; 0 other;
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Query Match          70.4%; Score 617.8; DB 22; Length 1686;
Best Local Similarity 99.7%; Pred. No. 5.7e-133;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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PT Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
PS Claim 37; Page 212-213; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13 proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX
SQ Sequence 1686 BP; 407 A; 379 C; 388 G; 512 T; 0 other;

Query Match 70.4%; Score 617.8; DB 22; Length 1686;
Best Local Similarity 99.7%; Pred. No. 5.7e-133;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 15
AAS59974
ID AAS59974 standard; cDNA; 1692 BP.
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AC AAS59974;
XX
XX 29-JAN-2002 (first entry)
XX Canine IL-13R/IgG-Fc fusion protein cDNA nCaIL-13Ralpha2-Fc-B9 1689.
XX
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
XX IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
XX immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX immune response.
XX
XX Canis familiaris.
XX WO200177332-A2.
XX
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US11498.
XX
XX 07-APR-2000; 2000US-195659P.
XX 07-APR-2000; 2000US-195874P.
XX
XX (HESK-) HESKA CORP.
XX
XX McCall CA, Tang L;
XX
XX WPI; 2001-657172/75.
XX P-PSDB; AAU69140.
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G
XX protein or canine interleukin-13 receptor protein useful for regulating
XX immune response of an animal and for developing regulatory compounds -
XX
XX Claim 37; Page 200-203; 221pp; English.
XX
XX The invention concerns an isolated canine protein, preferably canine
XX immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
XX receptor protein, the nucleic acids encoding them, antibodies
XX raised against them, fusion proteins between the IgG and IL-13 proteins
XX and methods of isolating regulators of them. The regulators are useful
XX for regulating an immune response in a canine. The proteins useful to
XX develop regulatory compounds including inhibitors and activators that,
XX when administered to a canine in an effective manner, are capable of
XX protecting canine from disease mediated by IL-13Ralpha or IL-13. The
XX regulators are useful for treating canine IgG (heavy and/or light chain)
XX and/or canine IL-13R mediated responses. The molecules of the invention
XX are useful to regulate the immune response of an animal (e.g. by gene
XX therapy). The present sequence encodes a protein of the invention.
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XX Sequence 1692 BP; 518 A; 376 C; 385 G; 413 T; 0 other;

Query Match 70.4%; Score 617.8; DB 22; Length 1692;
Best Local Similarity 99.7%; Pred. No. 5.7e-133;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

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Scoring table: IDENTITY_NUC
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Searched: 1797656 seqs, 10463268293 residues
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Listing first 45 summaries

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- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	765	87.1	1095	6	AX280330	Sequence	
c	7	765	87.1	1095	6	AX280332	Sequence
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c	11	617.8	70.4	954	6	AX280335	Sequence
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14	617.8	70.4	1686	6	AX280345	Sequence	
c	15	617.8	70.4	1686	6	AX280347	Sequence
16	617.8	70.4	1692	6	AX280342	Sequence	
c	17	617.8	70.4	1692	6	AX280344	Sequence
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ALIGNMENTS

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AX280322.1	VERSION	AX280322.1	GI:16607700			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	ORGANISM					
1 (sites)	REFERENCE					
McCall,C.A. and Tang,L.	AUTHORS					
Compositions and methods related to canine igg and canine il-13 receptors	TITLE					
Patent: WO 0177332-A 57 18-OCT-2001;	JOURNAL					
Heska Corporation (US)						
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DEFINITION AX280324
ACCESSION AX280324
VERSION AX280324.1 GI:16607702
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 59 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
source
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/db_xref="taxon:9615"
BASE COUNT 273 a 165 c 141 g 298 t 1 others
ORIGIN

Query Match 99.9%; Score 877; DB 6; Length 878;
Best Local Similarity 100.0%; Pred. No. 1.8e-166;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
 AF314533
 LOCUS
 DEFINITION
 Canis familiaris interleukin 13 receptor alpha chain 2 (IL13Ra2)
 mRNA, complete cds.
 ACCESSION
 VERSION
 AF314533
 AF314533.1 GI:16151870
 KEYWORDS
 SOURCE
 dog.
 ORGANISM
 Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 AUTHORS
 Tang, L.
 TITLE
 Molecular cloning of canine IL-13 receptor alpha chain (alpha and
 alpha2) cDNAs and detection of corresponding mRNAs in canine
 tissues
 JOURNAL
 MEDLINE
 21287533
 PUBMED
 11389954
 REFERENCE
 2 (bases 1 to 1454)
 Tang, L.
 Direct Submission
 Submitted (18-OCT-2000) Allergy and Immunology, Heska Corporation,
 1613 Prospect Parkway, Fort Collins, CO 80525, USA
 JOURNAL
 Location/Qualifiers
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 491 a 238 c 282 g 442 t 1 others

3' UTR
 BASE COUNT
 ORIGIN

Query Match 99.9%; Score 877; DB 4; Length 1454;
 Best Local Similarity 100.0%; Pred. No. 1.6e-166;
 Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 caaggaaatcggaagaaactaaataatcaagatatggactgtgtatatatacaactggcaatat 60
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 Db 1417 TGAATAAATCTTATTTTAAANGAAAAA 1454

RESULT 4
 AX280325
 LOCUS
 DEFINITION
 Sequence 60 from Patent WO0177332.
 ACCESSION
 AX280325
 VERSION
 AX280325.1 GI:16607703
 KEYWORDS
 dog.
 SOURCE

ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 60 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
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/organism="Canis familiaris"
/db_xref="taxon:9615"
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BASE COUNT 491 a 238 c 282 g 442 t 1 others
ORIGIN

Query Match 99.9%; Score 877; DB 6; Length 1454;
Best Local Similarity 100.0%; Pred. No. 1.6e-166;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1417 TGAATAAATCTTATTTTAAANGAAAAA 1454
RESULT 5
AX280327/c
LOCUS AX280327 Sequence 62 from Patent WO0177332.
DEFINITION AX280327
ACCESSION AX280327
VERSION AX280327.1 GI:16607705
KEYWORDS dog.
SOURCE
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 62 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 99.9%; Score 877; DB 6; Length 1454;
Best Local Similarity 100.0%; Pred. No. 1.6e-166;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
LOCUS AX280330 1095 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 65 from Patent WO0177332.
ACCESSION AX280330
VERSION AX280330.1 GI:16607708
KEYWORDS
SOURCE
  dog.
  Canis familiaris
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
  1 (sites)
  McCall,C.A. and Tang,L.
  Compositions and methods related to canine lgg and canine il-13
  receptors
  Patent: WO 0177332-A 65 18-OCT-2001;
  Heska Corporation (US)
  Location/Qualifiers
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BASE COUNT
ORIGIN
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Query Match 87.1%; Score 765; DB 6; Length 1095;
Best Local Similarity 100.0%; Pred. No. 5.1e-144;
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 tactggttatgagggcttgagccattccagcagagtgactgattacatcaagggttaatgga 180
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RESULT 7
AX280332/c
LOCUS AX280332 1095 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 67 from Patent WO0177332.
ACCESSION AX280332
VERSION AX280332.1 GI:16607710
KEYWORDS
SOURCE
  dog.
  Canis familiaris
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
  1 (sites)
  McCall,C.A. and Tang,L.
  Compositions and methods related to canine lgg and canine il-13
  TITLE
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Db 1114 TTTTCATCAAAAAAGAGCTTTTCTCATCAAGACACATTCTCT 1158

RESULT 9
AX280329/c AX280329 1158 bp DNA linear PAT 02-NOV-2001
LOCUS
DEFINITION Sequence 64 from Patent WO0177332.
ACCESSION AX280329
VERSION AX280329.1 GI:16607707
KEYWORDS
SOURCE
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 64 18-OCT-2001;
Heska Corporation (US)
FEATURES
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BASE COUNT 353 a 224 c 201 g 380 t
ORIGIN

Query Match 87.1%; Score 765; DB 6; Length 1158;
Best Local Similarity 100.0%; Pred. No. 5e-144;
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caaggaatcggaacataaaatcaagatatggactgtgtatattacaactggcaatat 60
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RESULT 10
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LOCUS
DEFINITION Sequence 68 from Patent WO0177332.
ACCESSION AX280333
VERSION AX280333.1 GI:16607711
KEYWORDS
SOURCE
ORGANISM
dog.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 68 18-OCT-2001;
Heska Corporation (US)
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BASE COUNT 329 a 162 c 192 g 271 t
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Query Match 70.4%; Score 617.8; DB 6; Length 954;
Best Local Similarity 99.7%; Pred. No. 1.8e-114;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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LOCUS
DEFINITION Sequence 70 from Patent WO0177332.
ACCESSION AX280335
VERSION AX280335.1 GI:16607713
KEYWORDS
SOURCE
dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 70 18-OCT-2001;
Heska Corporation (US)
FEATURES
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ORIGIN
Query Match 70.4%; Score 617.8; DB 6; Length 954;
Best Local Similarity 99.7%; Pred. No. 1.8e-114;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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LOCUS
DEFINITION Sequence 71 from Patent WO0177332.
ACCESSION AX280336
VERSION AX280336.1 GI:16607714
KEYWORDS
SOURCE
dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 71 18-OCT-2001;
Heska Corporation (US)
FEATURES
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ORIGIN
Query Match 70.4%; Score 617.8; DB 6; Length 1686;
Best Local Similarity 99.7%; Pred. No. 1.6e-114;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caaggaaatcgggaactaaattcaagatatgactgtgtatatcaaacaggcaatat 60
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Db 334 CAAGGAAATCGGAAACTAAAATTAAGATATGAGTGTGTATATACAACTGCAATAT 393
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:51:06 ; Search time 14.67 Seconds
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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13	313	14.7	396	2	US-08-939-727-14
14	312	14.6	420	1	US-07-757-390-13
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25	266	12.5	415	2	US-08-939-727-5
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ALIGNMENTS

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; Sequence 4, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whittiers, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-609-572-4

Query Match 70.5%; Score 1503; DB 1; Length 380;
Best Local Similarity 72.9%; Pred. No. 2,4e-138;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

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; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841.751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-841-751-4
Query Match 70.5%; Score 1503; DB 4; Length 380;
Best Local Similarity 72.9%; Pred. No. 2.4e-138;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;
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QY 120 SSWAETTYTWSPOGNETKIOMDCVYNNWQYLVCWSWPGMGVHEDTNYQLFYWYEGLDH 179
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RESULT 3
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; Sequence 4, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846.340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-4

Query Match 70.5%; Score 1503; DB 4; Length 380;
Best Local Similarity 72.9%; Pred. No. 2.4e-138;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

QY 1 MAFTHLDVGFYTLVCTAFG-SMLSNAEIKVNPQDFEIVDPGVLGYSLOWQPPPLPD 59
DB 1 MAFVCLAIGCLYTLISTTGTCTSSSTEIKVNPQDFEIVDPGVLGYSLOWQPPPLSLD 60
QY 60 NFKECTIEYELKYRNIDSENKTKITITKNLHYKDGFDLNKGIEAKINTLLPACQTNSEVR 119
DB 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNKGIEAKIHTLLPWOCTNGSEVQ 120
QY 120 SSWAETTYWSPQGNRETKIQDMDCVYNNWQYLVCSSKPGMGVHFDNYQLFYWYEGLDH 179
DB 121 SSWAETTYWSPQIGIPETKVQDMDCVYNNWQYLVCSSKPGIGVLLDNTNLYNLFYWYEGLDH 180
QY 180 SAECTDIKYNGKMGCRFPYLESSDYKDFYICVNGSSEOPRPSYFIFOLQNVKPM 239
DB 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNVKPLP 240
QY 240 PDYLSLVKNSEENLKNMKGPIPAKCFYIEFTEDGTWTTVTVEIQITRTSNE 299
DB 241 PVYLTFRESSCEIKLWSIPLGPAPARCFDYEIREDDTTLVATVENETYLKTNE 300
QY 300 SOKLCFLVRKVNICYSDDGIIWSEWSDQCKWG-DINKETLVFLIPAFVSIYVITC 358
DB 301 TRQJCFVVRKVNICYSDDGIIWSEWSDQCKWEGEDLSKTLLEWLPFGFILLVIFVTG 360
QY 359 LLLYKQKRALKTI 371
DB 361 LLLRKPNTPYKMI 373

RESULT 4

US-08-846-344-4
Sequence 4, Application US/08846344
Patent No. 6268480
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,344
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-344-4

Query Match 70.5%; Score 1503; DB 4; Length 380;
Best Local Similarity 72.9%; Pred. No. 2.4e-138;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

QY 1 MAFTHLDVGFYTLVCTAFG-SMLSNAEIKVNPQDFEIVDPGVLGYSLOWQPPPLPD 59
DB 1 MAFVCLAIGCLYTLISTTGTCTSSSTEIKVNPQDFEIVDPGVLGYSLOWQPPPLSLD 60
QY 60 NFKECTIEYELKYRNIDSENKTKITITKNLHYKDGFDLNKGIEAKINTLLPACQTNSEVR 119
DB 61 HFKECTVEYELKYRNIGSETWKTITITKNLHYKDGFDLNKGIEAKIHTLLPWOCTNGSEVQ 120
QY 120 SSWAETTYWSPQGNRETKIQDMDCVYNNWQYLVCSSKPGMGVHFDNYQLFYWYEGLDH 179
DB 121 SSWAETTYWSPQIGIPETKVQDMDCVYNNWQYLVCSSKPGIGVLLDNTNLYNLFYWYEGLDH 180
QY 180 SAECTDIKYNGKMGCRFPYLESSDYKDFYICVNGSSEOPRPSYFIFOLQNVKPM 239
DB 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQNVKPLP 240
QY 240 PDYLSLVKNSEENLKNMKGPIPAKCFYIEFTEDGTWTTVTVEIQITRTSNE 299
DB 241 PVYLTFRESSCEIKLWSIPLGPAPARCFDYEIREDDTTLVATVENETYLKTNE 300
QY 300 SOKLCFLVRKVNICYSDDGIIWSEWSDQCKWG-DINKETLVFLIPAFVSIYVITC 358
DB 301 TRQJCFVVRKVNICYSDDGIIWSEWSDQCKWEGEDLSKTLLEWLPFGFILLVIFVTG 360
QY 359 LLLYKQKRALKTI 371
DB 361 LLLRKPNTPYKMI 373

RESULT 5

US-08-609-572-2
Sequence 2, Application US/08609572
Patent No. 5710023
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-609-572-2

Query Match 59.6%; Score 1271.5; DB 1; Length 383;
Best Local Similarity 57.2%; Pred. No. 8.9e-116;
Matches 222; Conservative 71; Mismatches 88; Indels 7; Gaps 3;

QY 1 MAFIHLVGFLLVLCVAFGSMLSNAETKVNPPQDFEIVDPGYLGYSLOWQPPFLPDN 60
Db 1 MAFVH--IRCLCFILLCTITGYSL--EIKVNPQDFEILDPLGLLYLQWKPPVIEK 55

QY 61 FKECTIEVELKRYNDSENWKTIIITKNLHYKDGFDLNGIEAKINTLLPAQCTNGSEVRS 120
Db 56 FKGCILEVELKRYNVDSDSWKTIITRNLYKDGFDLNGIEGKIRTHLSEHCTNGSEVQS 115

QY 121 SWAETTYTSPGNETRTKIQDMDCVYNNQYLVCSWKKPGMVHFDNTYOLFVYEGLDHS 180
Db 116 PWIEASYGISDGSLETKIQDMKCIYNNQYLVCSWKKPGKTVSDNTYTMFFWYEGLDHA 175

QY 181 ACCTDYIKVNGKMGCRFPYLESSDYKDFYICVNGSSSQIPRSPYFFIQLONIVKPMPP 240
Db 176 LQCADYLQHDEKNVCKLSNLDSSDYKDFICVNGSSKLEPIRSTYTFQLNIVKPLPP 235

QY 241 DYLSLTVKNSSEINKLWNKPKGPIPAKCFIYEIETEDGTTWVTTTVEINEIOITRTSNES 300
Db 236 EFLHISVENSIDIRKMWSTPGGPPIPRCVTYEIVIREDDISWESATDKNDMLKRRANES 295

QY 301 QKLCFLVRSKVNIYCSDDGINSWSEDEQCWKGDINWETLVFLFIPFAFVSIFVLVITCLL 360
Db 296 EDLCFFVRCKVNIYCADDGINSWSEEECEWEGYTGPDSKIIFIVPVCVLCFFIFLILLCLLI 355

QY 361 LYKQALLKTIPTHT--KKEVFSHQDTFC 386
Db 356 VEKEEPEPTLSLHVDLNLKEVCAYEDTLC 383

RESULT 6
US-08-841-751-2
; Sequence 2, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive

;
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841.751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 383 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-841-751-2

Query Match 59.6%; Score 1271.5; DB 4; Length 383;
Best Local Similarity 57.2%; Pred. No. 8.9e-116;
Matches 222; Conservative 71; Mismatches 88; Indels 7; Gaps 3;

QY 1 MAFIHLVGFLLVLCVAFGSMLSNAETKVNPPQDFEIVDPGYLGYSLOWQPPFLPDN 60
Db 1 MAFVH--IRCLCFILLCTITGYSL--EIKVNPQDFEILDPLGLLYLQWKPPVIEK 55

QY 61 FKECTIEVELKRYNDSENWKTIIITKNLHYKDGFDLNGIEAKINTLLPAQCTNGSEVRS 120
Db 56 FKGCILEVELKRYNVDSDSWKTIITRNLYKDGFDLNGIEGKIRTHLSEHCTNGSEVQS 115

QY 121 SWAETTYTSPGNETRTKIQDMDCVYNNQYLVCSWKKPGMVHFDNTYOLFVYEGLDHS 180
Db 116 PWIEASYGISDGSLETKIQDMKCIYNNQYLVCSWKKPGKTVSDNTYTMFFWYEGLDHA 175

QY 181 ACCTDYIKVNGKMGCRFPYLESSDYKDFYICVNGSSSQIPRSPYFFIQLONIVKPMPP 240
Db 176 LQCADYLQHDEKNVCKLSNLDSSDYKDFICVNGSSKLEPIRSTYTFQLNIVKPLPP 235

QY 241 DYLSLTVKNSSEINKLWNKPKGPIPAKCFIYEIETEDGTTWVTTTVEINEIOITRTSNES 300
Db 236 EFLHISVENSIDIRKMWSTPGGPPIPRCVTYEIVIREDDISWESATDKNDMLKRRANES 295

QY 301 QKLCFLVRSKVNIYCSDDGINSWSEDEQCWKGDINWETLVFLFIPFAFVSIFVLVITCLL 360
Db 296 EDLCFFVRCKVNIYCADDGINSWSEEECEWEGYTGPDSKIIFIVPVCVLCFFIFLILLCLLI 355

QY 361 LYKQALLKTIPTHT--KKEVFSHQDTFC 386
Db 356 VEKEEPEPTLSLHVDLNLKEVCAYEDTLC 383

RESULT 7
US-08-846-340-2
; Sequence 2, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori

APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846.340
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609.572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-2

Query Match 59.6%; Score 1271.5; DB 4; Length 383;
Best Local Similarity 57.2%; Pred. No. 8.9e-116;
Matches 222; Conservative 71; Mismatches 88; Indels 7; Gaps 3;
QY 1 MAFIHLDVGLTLLVCTAFGSMLSNAEIKVNPDPQDFEIVDPGCLGYSLOWQPPFLPDN 60
DB 1 MAFVH--IRCLCFILLCTITGYSL---EIKVNPDPQDFEILDPLGLGLYLQWKPPVIEK 55
QY 61 FKECTIEYELKYNRIDSNNKTIITKNLHYKDGFDLNGKIEAKINTLLPAACTNGSEVRS 120
DB 56 FKGTLEYELKYNRVDSDSWKTIITRNLYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQS 115
QY 121 SWAETTYTSPQGNRETKIQDMDCVYNNQYLVCSKPKMGVHFDNTNYOLFVWYEGLDHS 180
DB 116 PWIEASYGISDEGSLETQDMKCIYNNQYLVCSKPKGTYSNTYMTFFWYEGLDHA 175
QY 181 AECTDYIKVNGMCRFPYLESSDYKDFYICVNGSSSEQSPRPSYFIQOLNIVKPMPP 240
DB 176 LQCADYLQHDEKNVCGKLSNLDSSDYKDFYICVNGSSKLEPRSSYTVFQOLNIVKPLPP 235
QY 241 DYLSLTVKNSEENLNKNWPKGPIPAKCFYIEFTEDGTTWTTTVEINEIQITRTSNES 300
DB 236 EFLHSIVENSIDIRMKWSTPGGPIPRCPTYEIVIREDDISWESATDKNDMKLKRANES 295
QY 361 LYKORALLKTIPT--KKEVESHOPTFC 386
DB 356 VEKEPEPTLSHLVDLNKEVAYEDTLC 383

RESULT 8
US-08-846-344-2
Sequence 2, Application US/08846344
Patent No. 6268480
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846.344
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609.572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-344-2
Query Match 59.6%; Score 1271.5; DB 4; Length 383;
Best Local Similarity 57.2%; Pred. No. 8.9e-116;
Matches 222; Conservative 71; Mismatches 88; Indels 7; Gaps 3;
QY 1 MAFIHLDVGLTLLVCTAFGSMLSNAEIKVNPDPQDFEIVDPGCLGYSLOWQPPFLPDN 60
DB 1 MAFVH--IRCLCFILLCTITGYSL---EIKVNPDPQDFEILDPLGLGLYLQWKPPVIEK 55
QY 61 FKECTIEYELKYNRIDSNNKTIITKNLHYKDGFDLNGKIEAKINTLLPAACTNGSEVRS 120
DB 56 FKGTLEYELKYNRVDSDSWKTIITRNLYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQS 115
QY 121 SWAETTYTSPQGNRETKIQDMDCVYNNQYLVCSKPKMGVHFDNTNYOLFVWYEGLDHS 180
DB 116 PWIEASYGISDEGSLETQDMKCIYNNQYLVCSKPKGTYSNTYMTFFWYEGLDHA 175
QY 181 AECTDYIKVNGMCRFPYLESSDYKDFYICVNGSSSEQSPRPSYFIQOLNIVKPMPP 240
DB 176 LQCADYLQHDEKNVCGKLSNLDSSDYKDFYICVNGSSKLEPRSSYTVFQOLNIVKPLPP 235
QY 241 DYLSLTVKNSEENLNKNWPKGPIPAKCFYIEFTEDGTTWTTTVEINEIQITRTSNES 300
DB 236 EFLHSIVENSIDIRMKWSTPGGPIPRCPTYEIVIREDDISWESATDKNDMKLKRANES 295
QY 301 QKLCFLVRKVNICYSDDGWSEWSEDEQCWKGDINWKTLLVFLIPPAFVSIFVLVITCLL 360

Db 296 EDLCFFVRCKVNIYACDDGIWSEWSECEWGYTGPDSKIIIFIVPVCLEFFIFLLLLCL 355
QY 361 LYKORALLTIFHT--KKEVFESHQDFC 386
Db 356 VEKEEPEPTLSLHVDLNVKEVCATEDTLC 383

RESULT 9
US-08-969-125-9
; Sequence 9, Application US/08969125B
; Patent No. 6143871
; GENERAL INFORMATION:
; APPLICANT: BONNEFOY, JEAN-YVES
; GAUCHAT, JEAN-FRANCOIS
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,125B
; FILING DATE: 12-NO. 6143871-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9625899.1
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-179
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 427 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-969-125-9

Query Match 14.9%; Score 318.5; DB 4; Length 427;
Best Local Similarity 25.5%; Pred. No. 7.8e-23;
Matches 105; Conservative 64; Mismatches 176; Indels 67; Gaps 19;

QY 11 LYTLLVCTAFGSMLSN-AEIKVNPDPDFIVDPGYLGLSLQWQPPLFPDNFKECTIEYE 69
Db 10 LWALLLCAGGGGGGAAATEQPPVNTLSVSVENLCTVIWTPNP--EGASSNCSLWY- 66
QY 70 LKYRNTSDSNWKTITITKNLHYKDGFDLNGKIEAKINTLL----PAQC-TNGSEVRSSWAE 124
Db 67 --FSHPGDKQDKKIAP-----ETRSIEVPLNERICLVGSGCSNSEKPSILVE 115
QY 125 TTYWTSPOQNRKTKIQDMCVYNNWQYLVCWKPGMGVHFDNYQLFYWYEGLDHSAECT 184
Db 116 KCI-SPPEGDPSAVTELOCIWHNLSYMKCSWLPGNTSPDNTYLYWHRSLKTHQCE 174
QY 185 DYIKVNGKNNGCRFPY--LESSDYKDFYICVNGSSSOPIRPSYFTFQLQNIKVKMPDPY 242
Db 175 NIFR-EGQVFGCSFDLTWKVDSFEGHSQIHWKDNAGIKFSPNVLPLTSRVKDPDPPI 233

QY 243 LSVTKNSEINLKNMMPKGPPIAKCFIYEIEFTDGTWTWTTTVEHIEQITRISNESOK 302
Db 234 KNLSPHN-DDLYVQWENPQNF-SRCLFYEVEVNS-----QTETHNVFYVQEAECENPE 286
QY 303 L-----CFLV-----RSKVNLYC-SDDGIWSEWSDQCQWKGDIWKETLV 340
Db 287 FERNVENTSCFMVPGVLPDPTLNTVRIRVTKNLCLYEDDKLWSNWSQEMSTGK---KRNST 343
QY 341 FFLIPFAFYSIFVL-VITCLLLYKORALLKTIFFHTK-----KEVFESHQD 383
Db 344 LYITMLLIVPVIVAGAIIVLLLYLKR--LKIIFFPPIDPGKIFKEMFGQDN 393

RESULT 10
US-07-757-390-14
; Sequence 14, Application US/07757390
; Patent No. 5453491
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,390
; FILING DATE: 19910910
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-757-390-14

Query Match 14.7%; Score 313; DB 1; Length 396;
Best Local Similarity 28.9%; Pred. No. 2.4e-22;
Matches 103; Conservative 62; Mismatches 156; Indels 36; Gaps 15;

QY 23 MLSNAEIKVNPDPDFIVDPGYLGLSLQWQPPLFPD-NFKECTIEYELKYRNIDSENK 81
Db 22 LLPDEKISLLPPVNFITKVTG-LAQVLLQWKN--PDQQRNVNLEYQVKINAPKEDDYE 78
QY 82 TITIKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRSSWAEITTYTSPQGNRETKIOD 141
Db 79 TRITES---KCVTILHKGFSAVRTLQ---NDHSLSSWASAEI-HAPPGSPGTSIVN 131
QY 142 MCVYNNWQ-----YLVCSWKPGMGVHFDNYQLFYWYEGLDHSAECTDIK-V 189
Db 132 LYTCTNTEDNYSRUSYQVSLHCTWLVTGDPEDQYFLYRYG--SWTECQCEYSDT 189

Qy	23	MLSNAETKVNPPQDFEIVDPGYGLYLSLQWQPPFLPPD--NFEKCTIEVELYKRNIDSENWK	81
Db	22	LLPEKTSLLPVPNTTKVTG--LAQVLLQKPN--PDEQRNVNLEYQVKNAPKEDDY	78
Qy	82	TIITKNLHYKPGFDLNKGIEAKINTLLPAQCTNGSEVRSSAETTYWTSPQGNRETKIQD	141
Db	79	TRITES---KCVTTLRHGFGASVETILQ---NDHSLAASWASAEI--HAPGSGPGTSIVN	131

QY	23	MLNSAEIKVNPQDFETVDPGYGLYSLOWQPPLFPD-NFKECTTEYELAYKRNIDSENWK	81
D6	22	LLPDEKISLLPVNFITTKVTG-LAQVLLQWKPN-PDQEQRNVLLEYQVKTNAPKEDDYE	78

Query Match 14.6%; Score 312; DB 1; Length 420;
Best Local Similarity 28.6%; Pred. No. 3.3e-22;

CT 707 244 000

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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 13:33:57 ; Search time 4150.53 seconds
(without alignments)
4728.209 Million cell updates/sec

Title: US-09-828-995B-60
Perfect score: 1454
Sequence: 1 ggcacagcgtgattgtg.....aaangaaaaaaaaaaaaa 1454

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	662.8	45.6	954	9 AL525497	AL525497 AL525497
2	641	44.1	928	9 AL562513	AL562513 AL562513
3	509.4	35.0	683	10 BG778615	BG778615 602668073
4	491.4	33.8	743	10 BG723203	BG723203 602690806
5	437.6	30.1	658	10 B1828427	B1828427 603078385
6	387.8	26.7	676	9 A1798934	A1798934 we94e04.x
7	349	24.0	926	10 BF620022	BF620022 601473366
8	346.2	23.8	715	10 BE788633	BE788633 601475992
9	320.2	22.0	445	9 AW954333	AW954333 EST366403
10	310.2	21.3	867	10 BF525412	BF525412 602069493
11	291	20.0	579	9 AW629184	AW629184 hi52b02.x
12	286.6	19.7	537	10 BF591502	BF591502 nab99a12.
13	271.2	18.7	649	10 BE289033	BE289033 601091625
14	264.4	18.2	365	9 AA298563	AA298563 EST141178
15	262.6	18.1	517	9 AW136614	AW136614 UI-H-BII-
16	261.4	18.0	476	10 BF443846	BF443846 261485 MA
17	248	17.1	379	10 BF443844	BF443844 261483 MA

c 18	233.8	16.1	506	9 AW236406	AW236406 xol59l2.x
c 19	231.4	15.9	479	9 AI358911	AI358911 qy19c05.x
c 20	230	15.8	443	9 AA909507	AA909507 oll16dl1.s
c 21	225.6	15.5	755	10 BE619361	BE619361 601473366
c 22	223.2	15.4	675	10 BE964459	BE964459 601658166
c 23	192.4	13.2	473	10 R52795	R52795 y999f10.t1
c 24	188.2	12.9	904	10 B1462644	B1462644 603203069
c 25	185.2	12.7	396	10 BG190222	BG190222 RST9279 A
c 26	184.4	12.5	399	10 BG213456	BG213456 RST33052
c 27	180.6	12.4	403	10 BG201950	BG201950 RST21296
c 28	180.4	12.4	409	10 BG215092	BG215092 RST34750
c 29	178	12.2	360	9 AA621766	AA621766 af06dl0.s
c 30	171	11.8	823	10 BF968964	BF968964 602270160
c 31	164.6	11.3	465	10 BF523126	BF523126 UI-R-C3-s
c 32	158.2	10.9	446	9 AW001800	AW001800 ws05c01.x
c 33	150.4	10.3	465	10 R52796	R52796 y999f10.s1
c 34	128.2	8.8	341	9 AA921043	AA921043 vy75h06.r
c 35	87.4	6.0	160	9 A1547789	A1547789 UI-R-C3-s
c 36	84.8	5.8	530	12 AZ557979	AZ557979 RPCI-23-1
c 37	69.6	4.8	176	12 AZ108580	AZ108580 RPCI-23-4
c 38	58	4.0	1101	12 CNS0039G	AL063921 Drosophil
c 39	58	4.0	1201	12 CNS016E1	AL106627 Drosophil
c 40	54.2	3.7	469	12 AQ761600	AQ761600 HS_3132_B
c 41	53.2	3.7	987	12 CNS014PQ	AL104456 Drosophil
c 42	53	3.6	928	12 CNS00DKY	AL071865 Drosophil
c 43	52.8	3.6	1043	12 CNS0145P	AL103735 Drosophil
c 44	52	3.6	1101	12 CNS00EVL	AL069706 Drosophil
c 45	50.8	3.5	928	12 CNS00DKY	AL071865 Drosophil

ALIGNMENTS

RESULT 1
AL525497 954 bp mRNA linear EST 13-FEB-2001
LOCUS LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC012YF21 5
DEFINITION prime, mRNA sequence.
ACCESSION AL525497
VERSION AL525497.1 GI:12788990
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 954)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..954
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC012YF21"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com
http://fulllength.invitrogen.com"
BASE COUNT 295 a 172 c 285 t 1 others

ORIGIN

Query Match 45.6%; Score 662.8; DB 9; Length 954;
Best Local Similarity 84.0%; Pred. No. 5.3e-105;
Matches 761; Conservative 0; Mismatches 142; Indels 3; Gaps 1;

QY 150 gagtggaaacttcaaaagtattgaatcttggaggaaatggctttcattcatttgatgtcgg 209
DB 44 GAGAGGCAATATCAAGGTTTAAATTCGGAGAAATGGCTTTGCTTGGCTGCTATCGG 103

QY 210 attcctctataccctgcttggtttggacagcatttgct---ctatgcttttcaaatgctga 266
DB 104 ATGCTTATATACCTTTCTGATAAGACACAACTTTGGCTGTACTTCTTTCAGACACCGA 163

QY 267 gataaaagttaactccctccagagatttggatagtagtggaccctggatattaggttatct 326
DB 164 GATAAAAGTTAACCCCTCAGGATTTGAGATAGTGGATCCCGGATACTTAGGTATCT 223

QY 327 ctcttggcaatggcaacctccattatttcgggataatttttaaggaatgcacaatagaata 386
DB 224 CTATTTGCAATGGCAACCCCACTGCTCTGGATCATTTTAAGGAATGCACAGTGAATA 283

QY 387 tgaattcaaataccgaaacattgatagtgaaacttggaaagaccatcattaccagaatct 446
DB 284 TGAACATAAATACCGAAACATTTGGTAGTGAACATGCAAGACCATCATTTACTAAGAATCT 343

QY 447 acattcaaaagtgggtttgatctcttaacaaagtattgaagcaaaagataaacaactct 506
DB 344 ACATTTACAAAGATGGTGTGATCTTTAACAAAGGCATTTGAAGCCGAAGATACACAGCTTT 403

QY 507 gccagcaaatgcacaaaatggatcagaagttagaagttcatggcgcaaaactacttattg 566
DB 404 ACCATGGCAATGCACAAATGGATCAGAAGTTCAAAAGTTCTCTGGGCAGAACTACTTATG 463

QY 567 gacatcaccaacaggaatcgggaaactaaaaatcgaagatgatgactgtgtattacaa 626
DB 464 GATATCACCACAAAGGAATTCACAGAACTAAAGTTTCAGGATATGGATGGCTATATACAA 523

QY 627 ctggcaatattagtcgtcttggaaacctggcatgggtgtccatttttgataccaatta 686
DB 524 TTGGCAATATTTACTCTGTCTTTGGAAACCTGGCATAGGTGTACTTCTTGATACCAATTA 583

QY 687 ccegttgttttactgtatgaggcttggaccatttcagcagagtgactgactgattacatcaa 746
DB 584 CAACTTGTTTTACTGTATGAGGCTTTGGATCATGCATTTACAGTGTGTTGATTTACATCAA 643

QY 747 ggttaattgaaaaaataatgggtatcgaggttccctcatttggagtcactcagactataaaga 806
DB 644 GGCTGATGCACAAATATAGGATGCGAGATTTCCTTATTTGGAGGCATCAGACTATATAAGA 703

QY 807 ttctacatctgtgttaattgggttcacagaatcccgaccttatcagaccagctattttat 866
DB 704 TTTCTATATTTGTTTAAATGGATCATCAGAGAACAAGCCCTATCAGATCCAGTTATTTTCAC 763

QY 867 ttttcagcttcaaaaataatagtttaaacctatgcacacagactaccttagtcttacttgaa 926
DB 764 TTTTTCAGCTTCAAAATATAGTTAAACCTTTTGGCCGACGCTATCTTTACTTCGGGA 823

QY 927 gaattcagaggaaataaactgaaatgggaacatgcgttaagggaccattccagccaaatg 986
DB 824 GAGTTTCATGAAATTTAAGCTGAATTTGGAGCATACCTTTTGGGACCTATTTCAGCAAGGTG 883

QY 987 ttctatttgaattgaattcagagaggtgttactacttctgggtgacttaccacagttga 1046
DB 884 TTTTGTATTTGAAATTTGAGATCAGAGAAGATGATACCTTGGTGACCTGCTACAGTTGA 943

QY 1047 gaatga 1052
DB 944 AAATGA 949

AL562513/c AL562513 928 bp mRNA linear EST 16-FEB-2001
LOCUS AL562513 LTI_NFL003_NBC3 Homo sapiens CDNA clone CSDDC012F21 3
DEFINITION prime, mRNA sequence.
ACCESSION AL562513
VERSION AL562513.1 GI:12911007
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 928)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 265 a 186 c 158 g 312 t 7 others
ORIGIN

Query Match 44.1%; Score 641; DB 9; Length 926;
Best Local Similarity 81.5%; Pred. No. 3.1e-101;
Matches 747; Conservative 6; Mismatches 161; Indels 3; Gaps 1;

QY 382 gaatatgaattaaaaatcacgaaacattgatagtgaaactgggaagccatcattaccacaa 441
DB 928 GGATWTTGAACATAATGACCGAAACATTGGTAGTGACACATGGAAGACCATCTACTAAG 869

QY 442 aatctacattacaagaatgggtttgatcttaacaaaggatttagaagcagaagataaaacaa 501
DB 868 AATCTACATAACAAACATGGGTTTGATCTTAACAAAGGCATTGAAGGAAAGACACACG 809

QY 502 ctctctccagcacaatgcacaaatggatcagaagtttagaagttcatggggcagaacactact 561
DB 808 CTTTTCACCATGGCAATGCACAAATGGATCGAAGTTCAAAGTTCTCTGGGCAGAACTACT 749

QY 562 tatggacatcacccacaaaggaaatcgggaaactaaataattcaagatatggactgtgtatat 621
DB 748 TATTTGGATATCACACACAGGAATTCAGAAACTAAAGTTTCAGGATATGGATTGCGTATAT 689

QY 622 tacaactggcaatatttagctctgctctctggaaacctggatgggtgccatttggatacc 681
DB 688 TACAATTGGCAATATTTTACTCTCTCTTGGAAACCTGGCATAGGTGTACTTCTTGATACC 629

QY 682 aattaccagttgttttactgggtatgagggccttggaccattcagcagagtgactgattac 741
DB 628 AATTACAACCTGTTTACTTGGTATGAGGGCTTGGATCATGCATTTACAGTGTGTGATTAC 569

QY 742 atcaaggttaatggaaaaaatatgggatcgaggtttccctatttggagtcacagactat 801
DB 568 ATCAAGGCTGATGGACAAAATATAGGATGAGATTTCCCTATTTTGGAGGCATCAGACTAW 509


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mRNA sequence.
BG723203
BG723203.1 GI:14002390
EST.
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 743)
NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: Miklos Palokovits, M.D., Ph.D.
CDNA library preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10732 row: 1 column: 02
High quality sequence stop: 730.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4823185"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-ttttttttttttttt-3',
size-selected for average insert size 2.2 kb and
normalized to 10^5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 229 a 135 c 164 g 214 t
ORIGIN
Query Match 33.8%; Score 491.4; DB 10; Length 743;
Best Local Similarity 84.5%; Pred. No. 2 le-75;
Matches 576; Conservative 0; Mismatches 102; Indels 4; Gaps 2;
QY 150 gagtggaaacttcaagattgaattgttgagggaattgggttcatttcatttggatgcgg 209
DB 49 GAGAGGCAATATCAGGTTTAAATCTCGAGAAATGGCTTTCGTTGCTTGCTATCGG 108
QY 210 attctctataccctgttctgtttgcacacacatttggct---ctatgctttcaaatgctga 266
DB 109 ATGCTTATATACCTTCTCATAGGACACACATTTGGCTCTACTTCTCATCTTCAGACACCGA 168
QY 267 gataaaagttaactcctccctcaggattttgagatagtgagccctgagatatttaggttatct 326
DB 169 GATAAAAGTTAACCTCTCCACGGA-TTTCAGATAGTGGATCCCGGATACATTAGGTTATCT 227
QY 327 ctcttggcaatggcaacctccattatttccgcgataaatttaagggaatgcacaaatagaata 386
DB 228 CTATTGGCAATGGCAACCCCACTGCTCTGGATCATTTTAAAGGAATGCACAGTGAATA 287
QY 387 tgaattaaataaccgaaacattgtagtgaacactggaagacacattaccacaaatct 446
DB 288 TGAACCTAAAATACCGAAACATTTGGTAGTGAACATGGAAGACCATCATTTACTAAGAATCT 347
QY 447 acattacaagaatgggtttgttcttaacaaaggattgaagcaagaataaacacattct 506
DB 348 ACATTACAAGATGGGTTTGATCTTAACAAGGGCATTTGAAGCGAAGATACACACGCTTTT 407
QY 507 gccagcacaatgcacaaatggtatcagaagttgaagttcatgtggcgagaactacttatty 566
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Db 408 ACCATGGCAATGCACAAATGGATCAGAACTTCAAAGTCTCTGGCGAGAACTACTTATNG 467
QY 567 gacatcacacaaggaatcgggaaactaaaattcaagatatgagctgtgtatatacaaa 626
Db 468 GATATCACCAACAGGAATTCACAGAACTAAAGTTTCAGGATATGGATTGGGTATATTACAA 527
QY 627 ctgggcaatttagtctgctctctggaaacctgagcatgggtgccatttgataccaattta 686
Db 528 TTGGCAATATTACTCTGTCTTGGAAACCTGGCATAGGTACTTCTTGTATACCAATTA 587
QY 687 ccagttgttttactggtatgagggcttggaccattcagcagagtgactgattacatcaa 746
Db 588 CAACCTGTCTTACTGTATGAGGCTTGGATCATGATCATGCTGTGTTGATTACATCAA 647
QY 747 ggttaattgaaaaataatcggatgcagggttccctctatttggagtcacagactataaaga 806
Db 648 GGCTGATGACAAAATATAGGATGCAGATTTCCTAATTTGGAGGCATCAGACTATAAGA 707
QY 807 ttctacatctgtgtaattggg 828
Db 708 TTCTATATATTGGTTTAATGG 729

RESULT 5
LOCUS BI828427
DEFINITION 603078385F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5170268 5',
mRNA sequence.
ACCESSION BI828427
VERSION BI828427
KEYWORDS EST.
SOURCE BI828427.1 GI:15939977
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 658)
NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA library preparation: Life Technologies, Inc.
CDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11423 row: 1 column: 21
High quality sequence stop: 651.
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/db_xref="taxon:9606"
/clone="IMAGE:5170268"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
BASE COUNT 202 a 121 c 141 g 194 t
ORIGIN
Query Match 30.1%; Score 437.6; DB 10; Length 658;
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Best Local Similarity 84.28; Pred. No. 4.3e-66; Matches 529; Conservative 0; Mismatches 94; Indels 5; Gaps 3;									
Qy	164	aagattgaacttggaggaatggtttcattcatttgatgttgatgtctctataacc	223						
Db	28	AAGTTTAAATCTCGGAGAAATGCTTTCGTTGCTTGGCTATCGGATGCTTATATACCT	87						
Qy	224	tgctgtttgcacagcatttggct---ctatgctttcaaatgctgagataaagtaacc	280						
Db	88	TTCTGATAAGCACACATATTTGGCTTACTTTCATCTTCAGACACCGAGATAAAGTTAAC	147						
Qy	281	ctctcaggatttgagataatggaacctggtatatttaggttatctctcttgaatggc	340						
Db	148	CTCCTCAGGA-TTTCAGATAGTGGATCCGGATACCTTAGGTATCTCTATTGGCAATGGC	206						
Qy	341	aacctcattattccggaatatttaaggaatgcacataagaataataataatacc	400						
Db	207	AACCCCACTCTCTGATCATTTTAAGGAATGCACAGTGGATATGAACATAAATACC	266						
Qy	401	gaacattgatagtgaaactggagaccatcattaccagaatctacattacaagatg	460						
Db	267	GAACATTTGGTAGTGAACATGGAAGACCATCTACTTAAGAATCTACATTACAAGATG	326						
Qy	461	ggtttgatcttaacaaaggtattgaagcaagataaaacacacttctgcagcacaaatga	520						
Db	327	GGTTTGATCTTAAAGGGCATTTGAAGCGAAGATACACACGCTTTTACCATGGCAATGCA	386						
Qy	521	caaatgagatcagaagttagaagttcatggcgagaaactacttattggacatcaccacaag	580						
Db	387	CAATGGATCAGAGTTCAAGTTCCTGGCGAGAACTACTTATGGATATACCCCAAG	446						
Qy	581	gaatcgggaaactaaatccaagatatggactgtgtatatcaaacctggcgaatatttag	640						
Db	447	GAATTCAGAAACTAAAGTTTCAGGATATGGATTGCGTATATTACAATTTGCAATATTAC	506						
Qy	641	tctgctttgaaacctggcatgggtccatcttttgatatacaaatcaccagttg-ttttac	699						
Db	507	TCTGTTCTTGGAAACCTGGCATAGGTGACTTCTTGATACCAATTTACAACTTGTTTTTAC	566						
Qy	700	tggatagggcttggaccatcagcagatgtagctgattacataaagtttaagtgaata	759						
Db	567	TGGTATAGGGCTTGATTCATGTCATACAGTGTGTTGATTACATCAAGCTGATGCACAA	626						
Qy	760	aataggatcaggtttccctatttgg 787							
Db	627	AATATAGGATCGAGATTTTCCCTATTG 654							
RESULT 6									
AI798934/c									
LOCUS									
DEFINITION									
we94e04.xl Soares_NFL_T_GBC_SI Homo sapiens mRNA linear EST 18-DEC-1999									
IMAGE:2348766 3' similar to SW:II32_HUMAN Q14627 INTERLEUKIN-13									
RECEPTOR ALPHA-2 CHAIN PRECURSOR ;, mRNA sequence.									
AI798934									
ACCESSION									
VERSION									
AI798934.1 GI:5364406									
KEYWORDS									
EST.									
SOURCE									
Homo sapiens									
ORGANISM									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
1 (bases 1 to 676)									
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.									
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),									
Tumor Gene Index									
Unpublished (1997)									
CONTACT: Robert Strausberg, Ph.D.									
Email: craps-r@mail.nih.gov									
This clone is available royalty-free through LLNL ; contact the									
IMAGE Consortium (info@image.llnl.gov) for further information.									
Insert Length: 882 Std Error: 0.00									
Seq primer: -40UP from Gibco									
High quality sequence stop: 468.									
FEATURES									
source									
Location/Qualifiers									
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/lab_host="DH10B"									
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with									
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;									
Equal amounts of plasmid DNA from three normalized									
libraries (fetal lung NBHL19W, testis NHT, and B-cell									
NCLCGAP_GCB1) were mixed, and ss circles were made in									
vitro. Following HAP purification, this DNA was used as									
tracer in a subtractive hybridization reaction. The driver									
was PCR-amplified cDNAs from pools of 5,000 clones made									
from the same 3 libraries. The pools consisted of									
I.M.A.G.E. clones 297480-302087, 682632-687239,									
726408-728711, and 729096-731399. Subtraction by Bento									
Soares and M. Fatima Bonaldo.									
BASE COUNT 205 a 133 c 117 g 221 t									
ORIGIN									
Query Match 26.7%; Score 387.8; DB 9; Length 676;									
Best Local Similarity 76.5%; Pred. No. 1.7e-57;									
Matches 518; Conservative 0; Mismatches 147; Indels 12; Gaps 3;									
Qy	754	ggaaaaaataatgggagcaggtttccctatttggagtcacacataaaagtattctac	813						
Db	676	GGACACATATAGGATGCAGATTTCCCTATTTGGAGGCATCAGACTATAGAGATATCAT	617						
Qy	814	atctgtgtaattgggtcaggaatcccagcctatcacaccagctattttttttcag	873						
Db	616	ATTTCGTAAATGGATCATCAGAGAACGAGCCTATCAGATCCAGTTATTTCACTTCTGTCAG	557						
Qy	874	cttcaaaatatagttaaaccctatgccaccagactacccttagctcttactgtgaagaattca	933						
Db	556	CTTCAAAATATATAGTTAAACCTTTGGCGCAGTCTATCTTACTTCTCGGAGAGTTCCA	497						
Qy	934	gaggaaataacctgaaatggaacatgctaagaacccattccagcccaaatgtttcatt	993						
Db	496	TGTGAATTAAGCTGAAATGGAGCATACCTTTGGGACCTATTTCCAGCAAGGTGTTTTGAT	437						
Qy	994	tatgaattgaattcacagagatggtactacttgggtgactcacaccagcttgagaaatgag	1053						
Db	436	TATGAATTTGAGATCAGAGAAAGATGATACCACCTTTGGTGACTGCTACACTTGAAATGAA	377						
Qy	1054	atacaaatcacagaacatcaaatgaaagcccaaaaattatgctttttgtgaagaagtaaa	1113						
Db	376	ACATACACCTTGAAACAAACAAATGAACCCGACAAATTATGCTTTGTAGTAAGAAGCAAA	317						
Qy	1114	gtgaattattgtctcagatgatggaatctgagatgagtgagtgatgaacaaatgctgg	1173						
Db	316	GTGAATATTATTGTCTCAGATGGCGGAAATTTGGAGTGGAGTGAGTAAAGCAATGCTGG	257						
Qy	1174	aaagtg---acatatgaaagaaaccttagtattttcttgataccatttctttgttc	1230						
Db	256	GAAGGTGAAACCTATCGAAGAAACCTTTGCTACGTTTCTGGCTACCATTTGGTTTCATC	197						
Qy	1231	tcaattattgttttggtaataacttgcctgtcttttggataaagcaagggctttactgaaa	1290						
Db	196	TTAATATTAGTTATATTGTAACCGCTGCTGCTTTTGGTAAAGCCAAACCCCTACCCAAA	137						
Qy	1291	acgat-----ctttcatacaaaaaaagaagctctttctcatcaagaacattctgttg	1343						
Db	136	ATGATTCCAGAAATTTTCTGTGATACATGAAGACTTTCCATATCAAGAGACATGTTATG	77						
Qy	1344	actcagtaacttgcagcttcttatggccagatgttaaatagcttatttaactgaagct	1403						
Db	76	ACTCAACAGTTTCCAGTC--ATGGCCAAATGTTCAATATGAGTCTCAATAAACTGAATTT	19						
Qy	1404	tttctcacaattatgaa 1420							

Query Match 23.8%; Score 346.2; DB 10; Length 715;
Best Local Similarity 77.5%; Pred. No. 2.4e-50;
Matches 526; Conservative 0; Mismatches 133; Indels 20; Gaps 8;

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Qy 394 aaataccgaacattgtagtgaacactggaagaccattaccacgaatctacattac 453
Db 5 AAATACCGAACAATGGTAGTGAACATGGGAAGCACTCATCTACTAAGAACTCATATTAC 64
Qy 454 aaagatgggttgattcttaacaaaggattgaagcaagaataaacacacactctgc---a 510
Db 65 AAAGATGGGTTTGATCTTTAAACAGGGCATTGAAGCGAAGATACACACGCCCTTTACCTAT 124
Qy 511 gcaaatgcacaaatggatca---gaagttagaagtctatggcgagaactactattg 566
Db 125 GCGCAATGGGCACAACTGGCATCAGCAAGTTTCAAAGTTTCCCTGGCGAGAAACTACTTATTG 184
Qy 567 gacatcaccacaaagaaatgggaactaaactaaactcaagatgactgtgtatatcaaa 626
Db 185 GATATCACCACAGAAATTCAGAAACTTAAAGTTTCAGAGATATGATTCGGTATATATACAA 244
Qy 627 ctggcaatatttagctgctcttgaaacacctggcatgggtgtccattttgtataccaatta 686
Db 245 TTGCAATATTTACTCTCTTCTTGAAACCTGGCATAGGTGCTACTTCTTGATACCAATTA 304
Qy 687 ccagttgttttactggtatgagggcttggaccattcagcagagtgactgattacaatcaa 746
Db 305 CAACCTTGTGTTTACTGGTATGAGGGCTTGGATCATGCATTCAGTGTGTCGATTACATCAA 364
Qy 747 ggttaatgaaaaaataatgagatggatcagggttccctatttggatgactcagactata-aag 805
Db 365 GCGTGATGGACAAAATATAGGATGCAGATTTCCCTATTTGGAGGCATCAGACTATACAA 424
Qy 806 attctaca---tctgtttaaagggtcatcagaatcccagcctatcagaccagctat 861
Db 425 ATTTCTATACTTGTCTGTTACACTGGATCATCAGAGAACAGCCTATCAGATCCAGTTAT 484
Qy 862 tt-tattttcagcttcaaaa---atatagttaaacctatgccacagacagactccttagct 917
Db 485 TTCCACTTTTTCAGCTTCAACATATACGCTTAAACCTATGCGCGAGCTATCTTACTTATA 544
Qy 918 tactgtgaagaattcagaggaaataaactgaaatggaactgcaatgcttaaaagga---cccat 974
Db 545 AACCTGGGAGAGTTTCATGTGAAATTAAGCTGACATGGGAGGATACCTACGGAGAGCCCTAT 604
Qy 975 tccagcceaattgtttatttattgaaattgaattcacagagatggttacttctgggtg-a 1033
Db 605 CCACCCAGGTCTACCGATCATGACATTCGGATCAGAGAGATGATGATACCTCCCTGGTGA 664
Qy 1034 ctaccagattgagaatga 1052
Db 665 CTGCTACAGTCGAAAATGA 683
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RESULT 9
AW954333
LOCUS AW954333 445 bp mRNA linear EST 01-JUN-2000
DEFINITION EST366403 MAGE resequences, MAGC Homo sapiens cDNA, mRNA sequence.
ACCESSION AW954333
VERSION AW954333.1 GI:8144016
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 445)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspar,R., Gay,C., Holt
I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 62

Seq primer: Reverse.
Location/Qualifiers
1. 445

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGC"
/note="vector: paluescriptSm"

BASE COUNT 137 a 77 c 88 g 143 t

Query Match 22.0%; Score 320.2; DB 9; Length 445;
Best Local Similarity 82.5%; Pred. No. 8.7e-46;
Matches 367; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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Qy 630 gcaatatttagctgctcttgaaacacctggcatgggtgtccattttgtataccaattacca 689
Db 1 GCAATATTTACTCTCTTCTTGAAACCTGGCATAGGTGCTACTTCTTGATACCAATTACAA 60
Qy 690 gttgttttactggtatgagggcttggaccattcagcagagtgactgattacaatcaaggt 749
Db 61 CTTGTTTTTACTGGTATGAGGGCTTGGATCATGCATTCAGTGTGTTGATTACATCAAGGC 120
Qy 750 taatgaaaaaataatgagatggatcagggttccctatttggatgactcagactataaagattt 809
Db 121 TCATGGACAAAATATAGGATGCAGATTTCCCTATTTGGAGGCATCAGACTATAAAGATT 180
Qy 810 ctacatctgtgttaatgggtcatcagaatcccagcctatcagaccagctattttatttt 869
Db 181 CTATATTTGTGTTAATGGATCATCAGAGAACAGCCTATCAGATCCAGTTATTTACCTTT 240
Qy 870 tcagcttcaaaaatagtttaaacctatgccacagacactaccttagtcttactgtgaaagaa 929
Db 241 TCAGCTTCAAAATATAGTTAAACCTTTGCGCGCAGCTATCTTACTTTTACTCGGGAGAG 300
Qy 930 ttcagaggaataatcaacctgaaatggaactgcaatgctcaaaagaccattccaagcaaatgttt 989
Db 301 TTCTATGTGAAATTAAGCTGAAATGGAGGATACCTTTTGGACCTATTTCCAGCAAGGTGTT 360
Qy 990 catttatgaattgaattcacagagatggttactacttgggtgactacacagcttgagaa 1049
Db 361 TGATTATGAATTTGAGATCAGAGAGAGATGATGATACCTTTGGTGGTACTGCTACAGTTGA 420
Qy 1050 tgagatacaaaatcacaagaacatca 1074
Db 421 TGAACATACACCTTTGAAAACAACA 445
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RESULT 10
BF525412
LOCUS BF525412 867 bp mRNA linear EST 11-DEC-2000
DEFINITION 602069493F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212574
ACCESSION 5', mRNA sequence.
VERSION BF525412
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 867)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.


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Db 279 AGTGAGTGAGTGATTAACAATGCTGGGAAGTGAAGACCTATCGAAGAAACTTTTGCTA 220
Qy 1204 ttttcttgatcaccattgtcttctgctcaataattgtttgttgtaataacttgcctgctt 1263
Db 219 CGTTTCGTGGCTACCATTTGGTTTCATCTTAATATAGTTATATTTGTAACCGGCTGCTT 160
Qy 1264 ttgtataagcaaaaggcttctactgaaacagat-----ctttcacaacaaaaagaagt 1316
Db 159 TTGGCTAAGCCAAACACCTACCCAAAATGATTCGACGAATTTTCTGTGATACATGAAGA 100
Qy 1317 cttttctcacaacacattcttgactcagtaactttcagctcttgccagatatt 1376
Db 99 CTTTCCATATCAAGAGACATGGTATGACTCAACAGTTTCCAGTC--ATGGCCAAATGTT 42
Qy 1377 aaatatgagcttattataaactgaagcttt 1405
Db 41 CAATATAAATCTCCATAAACTGAATTTT 13

RESULT 12
LOCUS BF591502/c
DEFINITION nab99a12.x1 NCI-CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3275807 3'
similar to SW:1132_HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2
CHAIN PRECURSOR ;, mRNA sequence.
ACCESSION BF591502
VERSION BF591502.1 GI:11683826
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 480.
FEATURES
Location/Qualifiers
source
1..537
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3275807"
/clone_lib="NCI-CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 161 a 108 c 94 g 170 t 4 others
ORIGIN

Query Match 19.7%; Score 286.6; DB 10; Length 537;
Best Local Similarity 74.8%; Pred. No. 5.2e-40;
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Matches 400; Conservative 0; Mismatches 123; Indels 12; Gaps 3;
Qy 883 atagttaaacctatgccaccagactaccttagcttactgtgaagaattcagagaaatt 942
Db 537 ATAGTTAAACCTTTGCCGCCAGTCTATCTTACTTTACTCGGAGAGTTCATGTGAATTT 478
Qy 943 aacctgaatggaacatgcctaaaggacccaccacaaatgtttctattatgaaatt 1002
Db 477 AAGCTGNAATGAGCANACCTTTGGGACCTATTTCAGCAAGGTGTTTGATTATGAATTT 418
Qy 1003 gaattcacagagatggttactacttgggtgactaccacagttgagaatgagatacaaatc 1062
Db 417 GAGATCAGAGAAGATGATACCTTGGTGNCTGCTAGTGTGAAATGAAACAGACACC 358
Qy 1063 acaagaacatcaaatgaaagccaaaattatgctttttgttaagaagtaaaagtgaattt 1122
Db 357 TTGAAACAACAATGAAACCGACAAATATGCTTTGTAGTAAGAAGCAAAAGTGAATTT 298
Qy 1123 tattgctcagatgaggaatctctgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1179
Db 297 TATTGCTCAGATGACGGAATTTGGAGTGAGTGGAGTGATTAACAATGCTGGGAAGTGAA 238
Qy 1180 gacatatgaaggaacaccttagtattttcttgataccattgttcttctcacaattt 1239
Db 237 GACCTATCGAAGAAACCTTTGCTACGTTCTGGCTACCATTTGGTTTGCATCTTAATATTA 178
Qy 1240 gttttggtataaacttgcctcttttgtataagcaaaaggcttttactgaaacagat---- 1295
Db 177 GTTATATTTGTAACCGGTCGCTTTGGGTAAAGCAACACCTACCCAAAATGATTCCA 118
Qy 1296 ---ctttcacaacaaaaagaagctctttctctcaatcaagacacacattctgttactcagtaa 1352
Db 117 GAATTTTCTGTGANACATGAAGACTTTCCATATCAAGAGACATGTTATTGACTCAACAG 58
Qy 1353 ctttcagctctatgccagatgttaaatatgagctcttattataaactgaagcttttc 1407
Db 57 TTTCCAGTC--ATGGCCAAATGTTCAATATGAGTCTCAATAAACTGAATTTTTC 5

RESULT 13
LOCUS BE289033
DEFINITION 601091625F1 NCI-CGAP_Mam5 Mus musculus cDNA clone IMAGE:3486223 5',
mRNA sequence.
ACCESSION BE289033
VERSION BE289033.1 GI:9169136
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM8522 row: a column: 08
High quality sequence stop: 513.
FEATURES
Location/Qualifiers
source
1..649
/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:3486223"
/clone_lib="NCI-CGAP_Mam5"
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RESULT 15
AW136614/c
LOCUS
DEFINITION
  UI-H-B11-aco-g-05-0-UI-s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
  IMAGE:2715080 3', mRNA sequence.
ACCESSION
  AW136614
VERSION
  AW136614.1 GI:6140747
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
  1 (bases 1 to 517)
  NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapsb-r@mail.nih.gov
  The sequence contained an oligo-dT track that was present in the
  oligonucleotide that was used to prime the synthesis of first
  strand cDNA and therefore this may represent a bonafide poly A
  tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
  NCI_CGAP clone distribution information can be found through the
  I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Seq primer: M13 Forward
  POLYA=yes.

FEATURES
      Location/Qualifiers
      1..517
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:2715080"
      /clone_lib="NCI_CGAP_Sub3"
      /lab_host="DH10B (Life technologies)"
      /note="vector: pT73D-Pac (Pharmacia) with a modified
      polylinker; Site_1: Not I; Site_2: Eco RI; The
      NCI_CGAP_Sub3 library is a subtracted library derived from
      the NCI_CGAP_Sub1 library, which is a subtracted library
      derived from B1. B1 constitutes a mixture of 21
      normalized or subtracted NCI_CGAP libraries: NCI_CGAP_C04
      , NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_C010,
      NCI_CGAP_C016, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
      NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
      NCI_CGAP_Br2, NCI_CGAP_C08, NCI_CGAP_CLL1, NCI_CGAP_Lei2,
      NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
      NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
      NCI_CGAP_Brn25. These 21 libraries were pooled and a
      single-stranded DNA preparation of the resulting mixture
      was used as a tracer in a subtractive hybridization with
      a driver whose composition is detailed below:
      NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683,
      3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775
      , 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342
      , 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831,
      1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
      LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,
      1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167,
      3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,
      1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1
      LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs
      985608-986759, 1101192-1101959, 1217928-1220615);
      NCI_CGAP_C010 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
      CloneIDs 1057416-1061255, 114584-1145351). Subtraction
      was performed as previously described (Bonaldo, Lennon &
      Soares (1996): Normalization and Subtraction: Two
      Approaches To Facilitate Gene Discovery. Genome Research
      6, 791-806.
      TAG_LIB=NCI_CGAP_Lu5
      TAG_TISSUE=lung
      TAG_SEQ=CAAC"
BASE COUNT      150 a      84 g      181 t

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ORIGIN

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Query Match      18.1%; Score 262.6; DB 9; Length 517;
Best Local Similarity 73.6%; Pred. No. 7.2e-36;
Matches 379; Conservative 0; Mismatches 124; Indels 12; Gaps 3;

Qy 920 ctgtgaagaattcagaggaataaacctgaaatgaagacatgcctaaagaccattccag 979
    || || || || || || || || || || || || || || || || || || || || ||
Db 517 CTCGGGAGAGTTCATGTGAATTAAGCTAAAATGAGCATACCTTTGGGACCTATTCCAG 458

Qy 980 ccaaatgtttctattgaattgaattcacagagatggtactacttgggggaatcacc 1039
    || || || || || || || || || || || || || || || || || || || || ||
Db 457 CAAGGTGTTTTCATTATGAATTTGAGATCAGAGAGATGATACCTTTGGTGGTACTGCTA 398

Qy 1040 cagttgagaatgagatacaaatcacagaacatcaatgaagcccaaaaattatgctttt 1099
    || || || || || || || || || || || || || || || || || || || || ||
Db 397 CAGTTGAAATGAACATACACCTTGAAACCAACAANAAGAAACCCGACAAATATGCTTTG 338

Qy 1100 tggtaagaagtaaaagtgaattatttctcagatgatggaatctggagtgagtgagtg 1159
    || || || || || || || || || || || || || || || || || || || || ||
Db 337 TAGTAAGAAGCAAAAGTGAATATTTATTGCTCAGATGACGGAATTTGGAGTGGAGTGG 278

Qy 1160 atgaacaatgctggaagaagt---gacatatggaagaaacaccttagtattttcttgatac 1216
    || || || || || || || || || || || || || || || || || || || || ||
Db 277 ATAAACAATGCTGGGAAGGTGAAGACCTATATCGAAGAAAACCTTTTGCTACGTTTCTGGCTAC 218

Qy 1217 catttgctttgtctcaatatttggtaataaactgcctgctcttttggatataagcaaa 1276
    || || || || || || || || || || || || || || || || || || || || ||
Db 217 CATTTGGTTTCATCTTAATATTAGTTATATTGTAACCGGTCTGCTTTTTCGCTAAGCCAA 158

Qy 1277 gggctttactgaaaacgat-----cttctacacaaaaaagaagctcttttctcatcaa 1329
    || || || || || || || || || || || || || || || || || || || || ||
Db 157 ACACCTACCCAAAATGATTCCAGAAATTTTCTGTGATACATGAAGACTTTCATATCAA 98

Qy 1330 gacacattctgtgactcagtaacttcaagctcttattggccagatgttaaatgatgctctt 1389
    || || || || || || || || || || || || || || || || || || || || ||
Db 97 GAGACATGGTATTGACTCAACAGTTTCCAGTC--ATGGCCAAATGTTCAATATGAGTCTC 40

Qy 1390 attaaactgaagcttttctcctcaaatattgaataaa 1424
    || || || || || || || || || || || || || || || || || || || || ||
Db 39 AATAAACTGAATTTTCTTCGCAAAAAAANAANA 5

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Search completed: September 23, 2002, 13:34:02
Job time: 9710 sec

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1503	70.5	380	1	IL132_HUMAN	Q14627 homo sapien
2	346	16.2	424	1	IL131_MOUSE	O09030 mus musculu
3	318.5	14.9	427	1	IL131_HUMAN	P78552 homo sapien
4	313	14.7	420	1	IL5R_HUMAN	Q01344 homo sapien
5	266	12.5	415	1	ILSR_MOUSE	P21183 mus musculu
6	256	12.0	831	1	PRUR_CHICK	Q04594 gallus gall
7	240.5	11.3	831	1	PRUR_MELGA	Q01094 meleagris g
8	232	10.9	369	1	IL3R_HUMAN	P31785 homo sapien
9	221	10.4	878	1	IL3B_MOUSE	P26954 mus musculu
10	221	10.4	896	1	CYRB_MOUSE	P28955 mus musculu
11	217.5	10.2	830	1	PRUR_COLL1	Q90374 columba liv
12	216	10.1	373	1	CYRG_CANFA	P40321 canis fami
13	208	9.8	369	1	CYRG_MOUSE	P34902 mus musculu
14	199	9.3	379	1	CYRG_BOVIN	O95118 bos taurus
15	195	9.1	581	1	PRUR_BOVIN	Q28172 bos taurus
16	194	9.1	610	1	PRUR_RAT	O05710 rattus norv
17	182	9.0	897	1	PRUR_HUMAN	P32927 homo sapien
18	189	8.9	608	1	PRUR_MOUSE	O08501 mus musculu
19	182.5	8.6	581	1	PRUR_CEREL	Q28235 cervus elap
20	180.5	8.5	630	1	PRUR_OREN1	P151513 oreochromis
21	178	8.3	616	1	PRUR_RABIT	P14787 oryctolagus
22	172.5	8.1	622	1	PRUR_HUMAN	P16471 homo sapien
23	154.5	7.2	917	1	IL6B_MOUSE	O00560 mus musculu
24	150	7.0	918	1	IL6B_HUMAN	P40189 homo sapien
25	145	6.8	918	1	IL6B_RAT	P40190 rattus norv
26	144.5	6.8	400	1	GMCR_HUMAN	P15509 homo sapien
27	139	6.5	862	1	IL2S_HUMAN	O99665 homo sapien
28	136.5	6.4	638	1	GHR_PIG	P19756 sus scrofa
29	131.5	6.2	378	1	IL3R_HUMAN	P28951 homo sapien
30	129	6.1	1282	1	DOME_DROME	Q9vwe0 drosophila
31	127.5	6.0	638	1	GHR_RABIT	P19941 oryctolagus
32	127.5	6.0	1630	1	GHR_PIG	P35992 drosophila
33	126	5.9	611	1	PRUR_COLL1	O90375 columba liv

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DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003532; Hematopo_receptor_S_F2.
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT DISULFID 184 197
FT CARBOHYD 115 115
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
SQ SEQUENCE 380 AA; 44176 MW; 36ACB1B5562C887 CRC64;

Query Match 70.5%; Score 1503; DB 1; Length 380;
Best Local Similarity 72.9%; Pred. No. 1.6e-118;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

QY 1 MAFIHLVGVFLVLTAVTAFG-SMLSNAEIKVNPQDFEIVDYGVLGSLQWQPPPLFPD 59
DB 1 MAFVCLAIGCLYELISTFGCTSSSDTEIKVNPQDFEIVDYGVLGSLQWQPPPLSLD 60

QY 60 NPECTIEYELKYNIDSENKWTITIKNLHYKDGDLNKGIEAKINTLLPAQCTNGSEVR 119
DB 61 HPKECTVEYELKYNIGSETWKTITIKNLHYKDGDLNKGIEAKIHTLLPWQCTNGSEVQ 120

QY 120 SSWAETTYTSPOGNETKIQDMCVYNNQYLVCSWPKMGVHFTNQLFYWYEGLDH 179
DB 121 SSWAETTYTSPOGNETKIQDMCVYNNQYLVCSWPKMGVHFTNQLFYWYEGLDH 180

QY 180 SAECTDYIKVNGKNGCRFPYLESSDYKDFYICVNGSSESQPIRPSYIFQLQNIKVP 239
DB 181 ALQCVDIYKADGONIGCRFPYLEASDYKDFYICVNGSSENKPIRPSYIFQLQNIKVP 240

QY 240 PYLSLTIVKNSINLKNMKGPIPAKCFIYEIEFTDGTWVTVTVENETQIRTSNE 299
DB 241 PYLVFTTRESSCEIKLWSIPGLPIPARCFYIEIREDDTTLVATVENETITLKTNE 300

QY 300 SOKLCFLVRKSVNIYCSDDGISENSDEQCKWG-DIWETLVFFLIPAFVSIFFLVITC 358
DB 301 TRQLCFVVRKSVNIYCSDDGISENSDEQCKWEGEDLSKRTLLRFLWLPFGFILLVIFVTG 360

QY 359 LLLYKORALLKTI 371
DB 361 LLLRKPNTYPKMI 373
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RESULT 2
ID IL13_MOUSE
AC O09030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (Interleukin-13 binding protein) (NR4).
DE IL13RA1 OR IL13RA OR IL13R.
GN IL13RA1 (Mouse),
OS Mus musculus (Mouse),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:9613964; PubMed:8552669;
RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Willson T.A.;
RT "Cloning and characterization of a binding subunit of the interleukin
```

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RT 13 receptor that is also a component of the interleukin 4 receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
CC -!- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
CC ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN
CC ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA
CC CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
CC GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY
CC SIMILARITY).
CC -!- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
CC IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, KIDNEY,
CC TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
CC EMBL: S80963; AAB50695.1; -.
CC MGI: 105052; IL13ral.
CC InterPro: IPR002996; CRIA.
CC InterPro: IPR003532; Hematopo_receptor_S_F2.
CC PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 25
FT CHAIN 26 424
FT DOMAIN 26 340
FT TRANSMEM 341 364
FT DOMAIN 365 424
FT DOMAIN 37 100
FT DISULFID 44 93
FT DISULFID 132 142
FT DISULFID 171 183
FT CARBOHYD 35 35
FT CARBOHYD 59 59
FT CARBOHYD 103 103
FT CARBOHYD 136 136
FT CARBOHYD 262 262
FT CARBOHYD 338 338
SQ SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9F9 CRC64;

Query Match 16.2%; Score 346; DB 1; Length 424;
Best Local Similarity 27.2%; Pred. No. 1.3e-21;
Matches 110; Conservative 71; Mismatches 175; Indels 48; Gaps 17;

QY 8 VGFYTLVCTAFGSMLSNAEIKVNPQDFEIVDYGVLGSLQWQPPPLFPDNFKECTIE 67
DB 7 LGELVLLLTATVGQVA-AATEVQPPVTNLVSVENLCTIITWSP--EGASPNCTLR 63

QY 68 YELKYRNDISENWKTIITIKNLHYKDGFDLNGIEAKINTLLPAQCTNGSEVRSSAEITY 127
DB 64 Y---FSHFDDQDDKKIAPET-HRKEELPDE---KICLVGQCSANESEKPSPLVKK 115

QY 128 WTSPOGNETKITQDMCVYNNQYLVCSWPKMGVHFTNQLFYWYEGLDHSAECTDYI 187
DB 116 ISPPGDPESAFTVTELCIWNLSYMKCSWLPGRNTSPDTHYTYWYSSLEKSRQENIY 175

QY 188 KVNKNMCMCRFPYLE---SSDYKDFYICVNGSSESQPIRPSYIFQLQNIKVPDPDYL 244
DB 176 R-EGQHIAICSEKLTKEVPSFEHQNVQIMVKNAGK--IRPSCKIVSLTSYKVPDPPIKH 232

QY 245 LTVKNSEENLKNMKGPIPAKCFIYEIEF--TEDGTTWVTVTVENETQIRTS-NE 301
DB 233 LLLKNG-ALLVQWKNPQN-FRSCLTUYEVEVNTQIDRHNILEVEDKQNSSESRNMBG 290

QY 302 KLCF-----LVRKSVNIYCSDDG-INSEWSDEQCKWGDINKE-TLVFFLIPF 346
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Db 291 TSCFQPGVLADAVTVRVVTKNLCDFDNDKLSWDSEAO----SIGKEQNSTFTYTM 346
Qy 347 AFVSIFVLVITCLLYKORALLKTF-----HTKKEVESHOD 383
Db 347 LTIPFVAVAVILLFLYLKRLKILIFPPIDPKGKIFKEMFGDQN 390

RESULT 3
IL131_HUMAN
ID IL131_HUMAN STANDARD; PRT; 427 AA.
AC P78552; O95656; O95646;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-
DE 13RA-1).
GN IL13RA1 OR IL13RA OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Carcinoma;
RX MEDLINE=97165986; PubMed=9013879;
RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,
RA Ferrara P.;
RT "Cloning of the human IL-13R alpha1 chain and reconstitution with the
RT ILAR alpha of a functional IL-4/IL-13 receptor complex.";
RL FEBS Lett. 401:163-166(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,
RA Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,
RA Eugster H.P., Bonnefoy J.Y.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=97067184; PubMed=8910586;
RA Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S.,
RA Leonard W.J.;
RT "cDNA cloning and characterization of the human interleukin 13
RT receptor alpha chain.";
RL J. Biol. Chem. 271:29265-29270(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
CC ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN
CC ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA
CC CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
CC GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.
CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
CC IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER,
CC SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND
CC KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
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CC EMBL; Y10659; CAA71669.1; -
DR EMBL; Y09328; CAA70508.1; -
DR EMBL; U62858; AAB37127.1; -
DR EMBL; U81379; AAD00510.3; -
DR HSSP; P40189; IBQU.
DR MIM; 300119; -
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hematopo_receptor_s_F2.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT CHAIN 1 21
FT SIGNAL 1 21
FT DOMAIN 22 427
FT TRANSMEM 344 367
FT DOMAIN 368 427
FT DOMAIN 39 102
FT DISULFID 46 95
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
FT CARBOHYD 265 265
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CARBOHYD 130 130
FT CONFLICT 358 358
SQ SEQUENCE 427 AA; 48759 MW; 5983B3E8F554107B CRC64;

Query Match 14.9%; Score 318.5; DB 1; Length 427;
Best Local Similarity 25.5%; Pred. No. 2.7e-19;
Matches 105; Conservative 64; Mismatches 176; Indels 67; Gaps 19;

Qy 11 LVTLLVCTAFGMLSN-AEIKVNPQDFEIVDPGYGLYLSLQWQPPFLPDFNKECTIEYE 69
Db 10 LWALLLCAGGGGGGAAPTQPPVTNLSVSVENLCTVIWTWNP--EGASSNCSLMY- 66
Qy 70 LKYRNIDSENWKTITKNLHYKDGFLNKGIEAKNTLL----PACQ-TNGSEVRSSNAE 124
Db 67 --FSHFGDKQDKKIAP-----ETRSIEVPLNERICLVQSGQCSNESEKPSILVE 115
Qy 125 TTYWTSPOGNRETKIQDMDCVYYNMQYLVCSSMKPGMVHFDNTNYQLFYWYEGLDHSAECT 184
Db 116 KCI-SPPEGDPESAVTELOCIWHNLSYKCSWLPGRNTSPDNTYLYWHRSLKIHQCE 174
Qy 185 DYIKYNGKMGCRFPY--LESSDYKDFYICVNGSSSQPIRPSYFIQNLQIVKMPDPY 242
Db 175 NIFR-EGOVFGCSFDLTVKVDSFSFQHSQVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHI 233
Qy 243 LSLTVKNSSEINLKNMKGPIPAKCFIYEIETEDGTWVTVTYVENEIQITRTSNESOK 302
Db 234 KNLSPHN-DLLXVQVENPQNF--SRCLFEYEVNNS-----QTETHNVFYVQEAECNPE 286
Qy 303 L-----CFLV-----RSKVNLYC--SDDGISWSEWDEQCQWKGIDINKETLV 340
Db 287 FERNVENTSCFMVPGVLPDPTLNTVIRVTKNKLCTEDDKLWSNQSQMSIGK---KRNST 343
Qy 341 FELIPFAFVSIFVL-VITCLLYKORALLKTFHTK-----KEVESHOD 383
Db 344 LVITMLIVPVIVAGIIVLLLYLKR--LKIIIFPPIDPKGKIFKEMFGDQN 393

RESULT 4
IL5R_HUMAN
ID IL5R_HUMAN STANDARD; PRT; 420 AA.
```

AC Q01344;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-5 receptor alpha chain precursor (IL-5R-alpha) (CD125 antigen).
GN IL5RA OR IL5R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9237767; PubMed=1495999;
RA Tavernier J., Tuytens T., Plaetinck G., Verhee A., Fiers W., Devos R.;
RT "Molecular basis of the membrane-anchored and two soluble isoforms of the human interleukin 5 receptor alpha subunit."; Proc. Natl. Acad. Sci. U.S.A. 89:7045-7045(1992).
RN [3]
RP SEQUENCE OF 1-335 FROM N.A. (S1 FORM).
RX MEDLINE=92005669; PubMed=1833065;
RA Tavernier J., Devos R., Cornelis S., Tuytens T., van der Heyden J., Fiers W., Plaetinck G.;
RT "A human high affinity interleukin-5 receptor (IL5R) is composed of an IL5-specific alpha chain and a beta chain shared with the receptor for GM-CSF."; Cell 66:1175-1184(1991).
RL Cell 66:1175-1184(1991).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN BINDS TO IL-5.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw125 entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm".
CC
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CC
CC EMBL; M96652; AAA59152.1; -
DR EMBL; M96651; AAA59151.1; -
DR EMBL; M75914; AAA36110.1; -
DR EMBL; A26249; CAA01793.1; -
DR EMBL; A24587; CAA01731.1; -
DR EMBL; A26251; CAA01794.1; -
DR PIR; A40267; A40267.
DR MIM; 147851; -
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003532; Hematoopo_receptor_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.
FT SIGNAL 1 20
FT CHAIN 21 420 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT DOMAIN 21 342 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 343 362 POTENTIAL.
FT DOMAIN 363 420 CYTOPLASMIC (POTENTIAL).
FT

FT CARBOHYD 35
FT CARBOHYD 131
FT CARBOHYD 216
FT CARBOHYD 244
FT VARSPLIC 335
FT VARSPLIC 336
FT VARSPLIC 333
FT VARSPLIC 333
FT VARSPLIC 334
SQ SEQUENCE 420 AA; 47700 MW; 420681FBC6B51700 CRC64;
Query Match 14.7%; Score 313; DB 1; Length 420;
Best Local Similarity 28.9%; Pred. No. 7.7e-19;
Matches 103; Conservative 62; Mismatches 156; Indels 36; Gaps 15;
QY 23 MLSNAEIKVNPQDFEIVDPGYLGLYSLOWQPPPLPD-NFKECTEYELKYNIDSENWK 81
DB 22 LLPDEKISLLPVPNFTIKVTG-LAQVLLQKPN--PDQQRNVNLEYQVKINAPKEDDYE 78
QY 82 TITKLNHYKDFDLNKGIEAKINTLLPAQCTNGSEVRSSWAETTYWTSPGNRETQKID 141
DB 79 TRITES---KCVTLHKGFSAVRILO---NDHSLASSWASAE-L-HAPPGSPGTSIVN 131
QY 142 MDCVYNNWQ-----YLVCSMKPGMGVHFDNTYQLFYWYEGLDHSAECTDYIK-V 189
DB 132 LTCTTNTTDDNYSRLRSYQVSLHCTWLVTGTDAPEDTQYELYRYG--SWTECQEVSKDT 189
QY 190 NGKNMGCRPP--YLBSSDYKDFYICVNGSSSQPRLPSYFIQLQNVKPMPPDYLSLV 247
DB 190 LGRNIACWPPRTFILLSKGRDLSVLVNGSSKSHARPDPQLFALHAIDQINPP--LNVT 247
QY 248 K-NSEINKLNWMPKGPAPKCFIYEIER--TEDGTTWTTTVENE-IOITRTSNESOKL 303
DB 248 ETEGRLSLQWKEKPSAFPIHCFDYEYKHTNRNGYLQIEKLTNAFISII---DDLSKY 304
QY 304 CFLVRKSVNIYSDGINSDEQCKWGDINKETLVFFLIPPAFVIFVLVITCL 360
DB 305 DVQVRAAVSSMCREAGLWSESQPIYVGNDEHKPLREWFVIVIMATICFILLISLI 361
RESULT 5
IL5R_MOUSE
ID IL5R_MOUSE STANDARD; PRT; 415 AA.
AC P21183;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Interleukin-5 receptor alpha chain precursor (IL-5R-alpha).
GN IL5RA OR IL5R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91092260; PubMed=2265612;
RA Takaki S., Tominaga A., Mita S., Sonoda E., Yamaguchi N., Takatsu K.;
RT "Molecular cloning and expression of the murine interleukin-5 receptor."; EMBO J. 9:4367-4374(1990).
RL EMBO J. 9:4367-4374(1990).
CC -!- FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN BINDS TO IL-5.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS. ALSO ON B-CELLS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
CC
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15  LVCTAFGSLNAEIKVNPQDFE---IVDPG-----YLCYLSIQWQPPLEP 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
101 ITVATNEIGSNS---SDQYVDVTSIVQSPGVNLLETKRSANIMYLWAKNSPPLLA 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
59  DNFECTEYELKYRNIDSENKWTITKNLHYKDGFDLNGKIEAKINTL-----LPAQ 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
157 DASSNHLHYELRIIPEKEEWETI-----SVGVQTCQKINRLNAGMRYVQVR 205
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
112 CTNGSEVRSSWAETTYWTSPQG-NRETQIDMDCVYVWQYLVCSWKPGMVHEDTYQL 170
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
206 CTLDPCGENSEWSESRHILLIPSGSPPEKPTTIKCRSPEKEFTTCWKGLDGGHPTNYTL 265
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
171 FYWYEGLDHSAECTYIKVNGKNMGCRFPYLESSYKDFYICVNGSSE--SQPIRSYFI 228

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15  LVCTAFGSLNAEIKVNPQDFE---IVDPG-----YLCYLSIQWQPPLEP 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
101 ITVATNEIGSNS---SDQYVDVTSIVQSPGVNLLETKRSANIMYLWAKNSPPLLA 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
59  DNFECTEYELKYRNIDSENKWTITKNLHYKDGFDLNGKIEAKINTL-----LPAQ 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
157 DASSNHLHYELRIIPEKEEWETI-----SVGVQTCQKINRLNAGMRYVQVR 205
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
112 CTNGSEVRSSWAETTYWTSPQG-NRETQIDMDCVYVWQYLVCSWKPGMVHEDTYQL 170
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
206 CTLDPCGENSEWSESRHILLIPSGSPPEKPTTIKCRSPEKEFTTCWKGLDGGHPTNYTL 265
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
171 FYWYEGLDHSAECTYIKVNGKNMGCRFPYLESSYKDFYICVNGSSE--SQPIRSYFI 228

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Db 266 LYSKEGEQVYECPDY--RTAGPN--SCYFDKKHTSEFTYINIVTRATNMGSSSDPHY-- 321
QY 229 FOLQNTVKKMPPDYLSTLVKNSEIN-----LKNWNP-----KGPFAKCFIYEIEF- 275
Db 322 VDVYIVQDPP--VNVTLKKPKPKRYLVLTNSPPPLADVRSGWLTLE---YELRLK 376
QY 276 TEDGTTWTTTVEINEIQITRTS--NESQKLCFLVRKSVNIYCSDD--GIWSESDQOCWK- 331
Db 377 PEEGSEWETIFVQQQYQKMSLPGKKYI-----IQIHCXPDHGSSESNSENYIOI 430
QY 332 -GDIWKETLVFLIPPAFVSIFVLVITCLLLYK 363
Db 431 PNDFRVKDMIVMIVGLVSLSLICLIMSWTWLVK 463

RESULT 7
PRLR_MELGA
ID PRLR_MELGA STANDARD; PRT; 831 AA.
AC Q91094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (TPRLR).
GN PRLR.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA MEDLINE=97057891; PubMed=8902221;
RA Zhou J.F., Zagworny D., Guemene D., Kuhnlein U.;
RT "Molecular cloning, tissue distribution, and expression of the
RT prolactin receptor during various reproductive states in Meleagris
RT gallopavo.;"
RL Biol. Reprod. 55:1081-1090(1996).
[2]
SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RC TISSUE=Ovary;
RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
RA Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L76587; AAB01544.1; .
CC DR EMBL; U22947; AAA75038.1; .
CC DR EMBL; U22924; AAA75039.1; .
CC DR HSP; F16471; I8P3.
CC DR InterPro; IPR002996; CRIA.
CC DR InterPro; IPR003961; FN.III.
CC DR Pfam; PF00041; fn3. 4.
CC DR SMART; SM00050; FN3. 3.
CC DR PROSITE; PS01352; HEMATOPO_REC_L_F1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831

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FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 91
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94394 MW; 220918320F77FAC1 CRC64;

Query Match 11.3%; Score 240.5; DB 1; Length 831;
Best Local Similarity 26.2%; Pred. No. 2.2e-12;
Matches 106; Conservative 53; Mismatches 154; Indels 91; Gaps 23;

QY 12 YTLVCTAFGSMLSNAEIKVNPDPDFE---IVDPG-----YLVYLSLQWQPP 55
Db 99 YNITV--TATNEIGSNS---SDPQYVDVTSIVQPGSPVNLTLTQRYANIMYLWAKWSP 153
QY 56 LPDFNFKECTIEVELKYRNIDSENKMTIITKNLHYKDGFDLANKGTEAKINTLLPAQCTNG 115
Db 154 LADASSNHYLYELRLKPEKEWETV-----PVGQVQCKINR--LNAGMRVY 201
QY 116 SEVR-----SSWAETTYTWS-----POGNRETKIQDMDCVYVYNWQYLVCSWKP 158
Db 202 VQVRCLMDPGWSE--WSSERRILISGGLSPXPETITK-----CRSPEKETFTCWKP 253
QY 159 GMGVHFDNRYQFYWVEGLDHAECTDYTKVGNKMGCRFPYLESDDYKDFICVNGSSE 218
Db 254 GLDGGHPTNYTLTLYSKEGEEQVYECPDY--RTAGPN--SCYFDKKHTSEFTYINIVTRATN 311
QY 219 --SQPIRPSYFIFOLQNIIVKMPDPDYLSLTGVKNSEIN-----LKNWNPCKPIPA---- 266
Db 312 MGSNSSDPHY--VDVYIVQDPPANVTLELK--PINKPKYMLMTWSP--PLADVRSG 365
QY 267 -KCFIYEIEF--TEDGTTWTTTVEINEIQITRTS--NESQKLCFLVRKSVNIYCSDD--GIW 321
Db 366 WLTLDELRLKPEEGEENETVFGQQTQYKMSLPGKKYI-----VQIHCXPDHGSW 419
QY 322 SEWSEDEQOCWK--GDIWKETLVFLIPPAFVSIFVLVITCLLLYK 363
Db 420 SEWSENYIEIPNDFRVKDMIVMIVGLVSLSLICLIMSWTWLVK 463

RESULT 8
CYRG_HUMAN
ID CYRG_HUMAN STANDARD; PRT; 369 AA.
AC P31785;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytokine receptor common gamma chain precursor (Gamma-C) (Interleukin-
DE 2 receptor gamma chain) (IL-2R gamma chain) (P64) (CD132 antigen).
GN IL2RG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92335883; PubMed=1631559;
RA Takeshita T., Asao H., Ohtani K., Ishii N., Kumaki S., Tanaka N.,
RA Munakata H., Nakamura M., Sugamura K.;
RT "Cloning of the gamma chain of the human IL-2 receptor.;"
RL Science 257:379-382(1992).
RN [2]

```

RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-93293887; PubMed=8514792;
 RA Noguchi M., Adelstein S., Cao X., Leonard W.J.;
 RT "Characterization of the human interleukin-2 receptor gamma chain
 gene.";
 RL J. Biol. Chem. 268:13601-13608(1993).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.
 RX MEDLINE-94004847; PubMed=8401490;
 RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,
 Willard H., Henthorn P.S.;
 RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated
 in X-linked severe combined immunodeficiency, SCIDX1.";
 RL Hum. Mol. Genet. 2:1099-1104(1993).
 RN [4]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE-94090315; PubMed=8266076;
 RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
 Arai K.-I., Sugamura K.;
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
 receptors for IL-2 and IL-4.";
 RL Science 262:1874-1877(1993).
 RN [5]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE-94090317; PubMed=8266078;
 RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguchi M.,
 Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
 Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 interleukin-4 receptor.";
 RL Science 262:1880-1883(1993).
 RN [6]
 RP IDENTIFICATION AS A IL-7R SUBUNIT.
 RX MEDLINE-94090316; PubMed=8266077;
 RA Noguchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
 Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 interleukin-7 receptor.";
 RL Science 262:1877-1880(1993).
 RN [7]
 RP 3D-STRUCTURE MODELING OF 57-248.
 RX MEDLINE-95111955; PubMed=7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 modelling.";
 RL Structure 2:839-851(1994).
 RN [8]
 RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
 RX MEDLINE-94130970; PubMed=8299698;
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
 de Saint Basile G.;
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
 severe combined immunodeficiency disease result in the loss of
 high-affinity IL-2 receptor binding.";
 RL Eur. J. Immunol. 24:475-479(1994).
 RN [9]
 RP VARIANT XSCID LYS-68.
 RX MEDLINE-94375038; PubMed=8088810;
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
 de Saint Basile G.;
 RT "Detection of three nonsense mutations and one missense mutation in
 the interleukin-2 receptor gamma chain gene in SCIDX1 that
 differently affect the mRNA processing.";
 RL Genomics 21:291-293(1994).
 RN [10]
 RP VARIANT XSCID HIS-162.
 RX MEDLINE-94300093; PubMed=8027558;
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
 Konno T., Maeda M., Uchiyama T., Sugamura K.;
 RT "Impairment of ligand binding and growth signaling of mutant IL-2
 receptor gamma-chains in patients with X-linked severe combined
 immunodeficiency.";

RL J. Immunol. 153:1310-1317(1994).
 RN [11]
 RP VARIANT XSCID ASN-39.
 RX MEDLINE-95029332; PubMed=7937790;
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
 de Saint Basile G.;
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X
 chromosome-linked severe combined immunodeficiency with peripheral T
 cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).
 RN [12]
 RP VARIANTS XSCID CYS-226 AND HIS-226.
 RX MEDLINE-95397841; PubMed=7668284;
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
 gene causing human X-linked severe combined immunodeficiency.";
 RL Am. J. Hum. Genet. 57:564-571(1995).
 RN [13]
 RP VARIANT XSCID SER-183.
 RX MEDLINE-96013903; PubMed=7557965;
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
 Levinsky R.L., Kinnon C.;
 RT "Screening for mutations causing X-linked severe combined
 immunodeficiency in the IL-2R gamma chain gene by single-strand
 conformation polymorphism analysis.";
 RL Hum. Genet. 96:427-432(1995).
 RN [14]
 RP VARIANT XSCID GLN-237 G-H-W INS.
 RX MEDLINE-95164726; PubMed=7860773;
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
 gamma-chain mutation causing X-linked severe combined
 immunodeficiency.";
 RL J. Clin. Invest. 95:895-899(1995).
 RN [15]
 RP VARIANT XSCID GLN-293.
 RX MEDLINE-95190013; PubMed=7883965;
 RA Schmalstieg F.C., Leonard W.J., Noguchi M., Berg M., Rudloff H.E.,
 Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a
 moderate form of X-linked combined immunodeficiency.";
 RL J. Clin. Invest. 95:1169-1173(1995).
 RN [16]
 RP VARIANT XSCID ARG-115.
 RX MEDLINE-97042245; PubMed=8900089;
 RA Stephan V., Wahn V., Le Deist F., Dirksen U., Broeker B.,
 Mueller-Fleckenstein I., Horneff G., Schroten H., Fischer A.,
 de Saint Basile G.;
 RT "Atypical X-linked severe combined immunodeficiency due to possible
 spontaneous reversion of the genetic defect in T cells.";
 RL New Engl. J. Med. 335:1563-1567(1996).
 RN [17]
 RP VARIANT XSCID GLN-285.
 RX MEDLINE-97295088; PubMed=9150740;
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
 Cant A., Kinnon C.;
 RT "B-cell-negative severe combined immunodeficiency associated with a
 common gamma chain mutation.";
 RL Hum. Genet. 99:677-680(1997).
 RN [18]
 RP VARIANT XSCID CYS-222.
 RX MEDLINE-98064061; PubMed=9399950;
 RA Sharfe N., Shahar M., Roifman C.M.;
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus
 morphology.";
 RL J. Clin. Invest. 100:3036-3043(1997).
 CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 INTERLEUKINS.
 CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED
 IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINEMIA, SWISS TYPE

```
CC OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -I- DATABASE: NAME=PROW; NOTE=CD guide Cdl32 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdl32.htm".
CC -I- DATABASE: NAME=IL2RBbase; NOTE=X-linked SCID mutation database;
CC WWW="http://www.nhgri.nih.gov/DIR/GMBB/SCID/".
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CC -----
CC EMBL: D11086; BAA01857.1; -
CC EMBL: L12183; AAA59145.1; -
CC EMBL: L12178; AAA59145.1; JOINED.
CC EMBL: L12176; AAA59145.1; JOINED.
CC EMBL: L12177; AAA59145.1; JOINED.
CC EMBL: L12179; AAA59145.1; JOINED.
CC EMBL: L12180; AAA59145.1; JOINED.
CC EMBL: L12181; AAA59145.1; JOINED.
CC EMBL: L12182; AAA59145.1; JOINED.
CC EMBL: L19546; AAC37524.1; -
CC DR PIR: A42565; A42565.
CC DR PDB: 1ILM; 26-JAN-95.
CC DR PDB: 1ILN; 26-JAN-95.
CC DR MIM: 308380; -.
CC DR MIM: 300400; -.
CC DR InterPro: IPR002996; CRIA.
CC DR InterPro: IPR003961; FN.III.
CC DR InterPro: IPR003531; Hematopo_receptor_S_F1.
CC -----
Query Match 10.9%; Score 232; DB 1; Length 369;
Best Local Similarity 24.1%; Pred. No. 3.9e-12;
Matches 65; Conservative 48; Mismatches 123; Indels 34; Gaps 9;
QY 125 TTVTWTSPQGNRET-----KIQDMDCVYVNWQYLVCWSKPGMGVHED 165
DB 25 TTTLT-PNGNEDTADFELTPTDLSVSTLPLPEVQCFVFNVMNCTNSSSEPP-Q 82
QY 166 TNYQLFYWYEGLDHS--AECTDYIKYNGKMGCRFPYLESSDYKDFYICVNGSSESQPIR 223
DB 83 TNLTLHWYKNSDNDKVKQSHVLFSEETSGCOLQKKEHLVQTFVVLQDPRE--PRR 140
QY 224 PSYFIFQLQNIKPMPPDYLSLVTKNSEELNKNWPKGPIPAKCFIYEIETFTD-GTTW 282
DB 141 QATQMLKQLNLVTPWAPENLT/LKLSSESQLELNN--NRFNLNHCLEHLVQYRTDWDHSW 197
QY 283 VTTTVEVEIQITRTSNESOK-LCFLYRSKVNIVCSDDGIWSEWSDQCWKGDINWETLVF 341
DB 198 TEGSDYIRKHFSLPSVDGQRRYTFVRYSRPNPLCGSAQHWSESHPIHNGSNFYSKRNPEL 257
QY 342 FLIPFAFVSI-----FVLVITCLLLYKQRAL 367
DB 258 FALAEAVVISVGSMLIISLLCYVFWLERTM 287
RESULT 9
IL3B_MOUSE STANDARD; PRT; 878 AA.
AC P26954;
DT 01-OCT-1993 (Rel. 27, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-3 receptor class II beta chain precursor (Colony
DE stimulating factor 2 receptor, beta 2 chain).
GN CSF2RB2 OR A12CA OR IL3RB2 OR IL3R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

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OX NCBI_TaxID=10090;
RP [1]
RX MEDLINE=90117145; PubMed=2404337;
RA Itoh N., Yonehara S., Schreurs J., Gorman D.M., Maruyama K., Ishii A.,
RA Yahara I., Arai K., Miyajima A.;
RT "Cloning of an interleukin-3 receptor gene: a member of a distinct
RT receptor gene family.";
RL Science 247:324-327(1990).
CC -I- FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3
CC RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE
CC OTHER CONTAINS THE BETA CHAIN ALSO SHARED BY HIGH-AFFINITY IL-5
CC AND GM-CSF RECEPTORS.
CC -I- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M29855; AAA39295.1; -
CC DR PIR: A40091; A40091.
CC DR MGD: MGI:1339760; Csf2rb2.
CC DR InterPro: IPR002996; CRIA.
CC DR InterPro: IPR000282; Cytok_receptor_2.
CC DR InterPro: IPR003961; FN.III.
CC DR Pfam: PF00041; fn3; 2.
CC DR SMART: SM00060; FN3; 2.
CC DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
CC KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 878 INTERLEUKIN-3 RECEPTOR CLASS II BETA
FT CHAIN EXTRACELLULAR (POTENTIAL).
FT DOMAIN 23 440 POTENTIAL.
FT TRANSMEM 441 462 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 463 878 BY SIMILARITY.
FT DISULFID 39 49 BY SIMILARITY.
FT DISULFID 78 95 BY SIMILARITY.
FT DISULFID 254 264 BY SIMILARITY.
FT DISULFID 293 310 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 878 AA; 97195 MW; 8EBC9092ADC24D56 CRC64;
Query Match 10.4%; Score 221; DB 1; Length 878;
Best Local Similarity 24.5%; Pred. No. 1e-10;
Matches 86; Conservative 58; Mismatches 155; Indels 52; Gaps 19;
QY 33 PPQDFEIVDPGLVGLSLQWQPPLPFDN---PKECTIEYELKYRNTDSNWKTIITKNLH 89
DB 139 PPKDTHISPSG--DHPFLLEWSVSLGDSQVSWLSKDIIEFVAYKRL-QSWED--ASSLH 193
QY 90 YKDGFDLNGIEAKI---NTLLPA-----QCTNGSEVR---SSWAETTYTSPQGNRETKI 139
DB 194 -TSNQVN--LEPKFLPNSIIVAAVRTRLISAGSLSGRPSRWSPEVHWDSQPGDK-AQP 249
QY 140 QDMDCVYVNWQYLVCWSKPGMGVHEDTNYQLFYWYEGLDHSAECTDYIKVNGKNM-----G 195
DB 250 QNLQCFDFDGIQSLHCSWEVMTQTGTSVSLGFLRPSPAAPEKSCSPVVPQAPQAVTRYR 309
QY 196 CRFPYLESSDYKDFYICVNGSSESQPIRSYFIFQLQNIKPMPPDYLSLVTKNSEELN 255
DB 310 CSLPVPPEPSAHSQYTVSVKHLGGKFIIMSYHI-----QMEPPILOT-KNRSYSYL 360
QY 256 KNNMKGPIPAKC-FIYEIETFTDGTWTWTTTVENEIQITRTS-----NBSQKLCFLVLRK 310
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Db 361 HWETOK--IPKYIDHTFQVQYKKKSESKDKSTENLGRVNSMDLPLEPDTSYCARVRVK 418
Qy 311 -VNIYCSDDGISEWSEDEQKGDWKEVLPFLIPFAFVSIFVLVITCLL 360
Db 419 PISDY---DGIWSENSNEYTWTQVMPPLWIVLI-----LVFLIFLILL 460

RESULT 10
CYRB_MOUSE
ID CYRB_MOUSE STANDARD; PRT; 896 AA.
AC P26955;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cytokine receptor common beta chain precursor.
GN CSF2RB OR CSF2RB1 OR AIC2B OR IL3RB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319131; PubMed=1695379;
RA Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yonehara S.,
RA Yahara I., Arai K., Miyajima A.;
RT "Cloning and expression of a gene encoding an interleukin 3 receptor-
RT like protein: identification of another member of the cytokine
RT receptor gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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CC
CC EMBL; M34397; AAA37204.1; .
DR PIR; A35782; A35782.
DR MGD; MGI:1339759; Csf2rb1.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR000282; Cytok_receptor_2.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 896
FT DOMAIN 23 441
FT TRANSMEM 442 463
FT DOMAIN 464 896
FT DOMAIN 132 241
FT DOMAIN 343 440
FT DISULFID 39 49
FT DISULFID 77 94
FT CARBOHYD 62 62
FT CARBOHYD 141 141
FT CARBOHYD 350 350
SQ SEQUENCE 896 AA; 99111 MW; 8CE16EDFDC07A999 CRC64;

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Query Match          10.4%; Score 221; DB 1; Length 896;
Best Local Similarity 22.6%; Pred. No. le-10;
Matches 90; Conservative 64; Mismatches 153; Indels 92; Gaps 21;

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Qy 31 VNPQDFEIVDPGYLG-----LSLQWQPPLPDPN----- 60
Db 100 VIPYTRFSTNEDYYSFRPDSLDGIQLMVLPAQNVQPP-L-PKNVSTSSSEDFLLEWSVS 158
Qy 61 -----FKECTIEYELKYNRIDSSENWKTITITKLNHYKDGFDLNGKIGIAKI----- 104
Db 159 LGDAQVSWLSSKDIIEFVAYKRL-QDSWED--AYSILH-TSKFQVN--PEPKLFLPNSIYA 212
Qy 105 ----NTLLPAQCTNGSEVRSSWAETTYTSPQGNRETKIQDDMDCVYNNQYLVCSWKPGM 160
Db 213 PRVTRFLYPGSSLSGRP--SRWSPEAHWDSQPGDK-AQPONLQCFDGLQSLHCSWEVWT 269
Qy 161 GVHFDNTYQLFYWYEGLDHSAECTDIYK-VNGKNM----GCRFPYLYESSDYKDFYICVNG 215
Db 270 QTTGVSFGLFYRPSVPAPEEKSCSPVVKPPGASVYTRYHCSLPVPEPSAHQSYTVSVKH 329
Qy 216 SSESQPIRSPYIFQLQNIIVKPMPPDYLSLTWNKSEINLKNWMPKGPPIPAKCFI---YE 272
Db 330 LEQGK-----FIMSYNHI--QMEPTLNLTKNRDSYSLHWETQK---MAYSFIEHTFQ 377
Qy 273 IEFTEDGTTWTTTVEINEIOITRTSNESQ---KLCFLVRSKVNICYDSDGIWSEWDEQC 329
Db 378 VOYKKSDSWEDSKTEN-LDRAHSMDSLSQLEPDTSCARVRVKPISNYDGIWSEWSEYT 436
Qy 330 WKGD-----IWKETLVFFLIPFAFVSIFVLVITCLLLYK 363
Db 437 WKTDVMVPTLWIVLIILVFLI---LTLILLRFGCVSVYR 472

RESULT 11
PRLR_COLLI
ID PRLR_COLLI STANDARD; PRT; 830 AA.
AC Q90374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cropsac;
RX MEDLINE=94283267; PubMed=75168666;
RA Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin
RT receptor.";
RL Endocrinology 135:269-276(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; U07694; AAA20646.1; .
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.

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KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 830
FT DOMAIN 24 439
FT TRANSMEM 440 460
FT DOMAIN 461 830
FT DOMAIN 25 122
FT DOMAIN 123 226
FT DOMAIN 229 326
FT DOMAIN 327 429
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
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FT CARBOHYD 304 304
FT CARBOHYD 316 316
FT CARBOHYD 336 336
FT SEQUENCE 830 AA; 94507 MW; 3B074B83CDF69EFF CRC64;

Query Match 10.2%; Score 217.5; DB 1; Length 830;
Best Local Similarity 25.7%; Pred. No. 1.8e-10;
Matches 87; Conservative 53; Mismatches 158; Indels 41; Gaps 16;

QY 47 YLSLQHPPLFPDPNFECTI-EYELKYRIDSNNKWTITKLNHYKDFGLNKGIKIAKN 105
Db 145 YLLAKWSPLPADVTSNSHYRYELRLKPEKEWETV---SVGVQTQKVNR-LOAGVK 200
QY 106 TLLPAQCTNGSEVRSSWAETTYTSPQ-NRETKIQDMDCVYNNMOYLYCSWKPGMGVHF 164
Db 201 YVVQVRCVLIDIGSEWSERHHIHNGESPPEKPIIKCRSPKETFTCWKPKSGDGGH 260
QY 165 DTNYQLFYWYEGLDHSAECTDIYKVNKNMGCRFPYLESSDYKDFYICVN-----GSSSES 219
Db 261 PTNYTLLYSKEGERVEYCPDY-KTAGPN-SCYFDKKHTSFMTIYNTIKATNEIGSNVS 318
QY 220 QPIRPSYFIFQLQNIKVPMPDYL---TVKNSEINLKNMMPKGPIPA-----KCFI 270
Db 319 DPL-----YVDYIYVQTPPVNVTLELAKTVNRKPYLVLTWSP--PLADVRSGWLTLD 371
QY 271 YEIEF--TEDGTTWTTTVEINEIQITRS--NESOKLFLVRSKVNIYCSDD--GIWSESD 326
Db 372 YELRLAPEAEWEETIFVGQTHYKMFSLNPGKKYI-----VQIHCKPDHGHGSWESWL 425
QY 327 EQCWK--GDIWKETLVFFLIPAFVSIFVLVITCLLLYK 363
Db 426 EKYLIQPTDFRIKDMVYWIIVGVLSLCLVMSWTMVLK 464

RESULT 12
CYRG_CANFA STANDARD; PRT; 373 AA.
AC P40321;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Cytokine receptor common gamma chain precursor (Gamma-C)
GN (interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=95130114; PubMed=7829104;
RA Henthorn P.S., Somberg R.L., Fimiani V.M., Puck J.M., Patterson D.F.,
RA Felsbush P.J.;
```

```
RT *IL-2R gamma gene microdeletion demonstrates that canine X-linked
RT severe combined immunodeficiency is a homologue of the human
RL disease."
CC Genomics 23:69-74 (1994).
CC -|- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -|- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
CC SEVERE COMBINED IMMUNODEFICIENCY.
CC -|- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY III-LIKE DOMAIN.
CC -|- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U04361; AAC48403.1; -.
CC HSSP; P31785; IILN.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 373
FT DOMAIN 23 261
FT TRANSMEM 262 283
FT DOMAIN 284 373
FT DOMAIN 151 249
FT DISULFID 62 72
FT DISULFID 102 115
FT CARBOHYD 24 24
FT CARBOHYD 71 71
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FT SEQUENCE 373 AA; 42516 MW; 03A0DE1F8B089D8B CRC64;

Query Match 10.1%; Score 216; DB 1; Length 373;
Best Local Similarity 25.1%; Pred. No. 8.7e-11;
Matches 70; Conservative 51; Mismatches 128; Indels 30; Gaps 11;

QY 104 INTLLPAQCTNGSE-----VRSSWAETTYTSPQNRKTIQDMDCVYNNMOYLYCSW 156
Db 23 LNSTVP--MPNGNEDITPDFFLTATPSETLSVSS-----LPLPEVQCFVFNVEYNNCTW 74
QY 157 KPGMGVHFDNTNYOLFVWYEGCL--DHSAACTDIYKVNKNMGCRFPYLESSDYKDFYICVN 214
Db 75 NSSSEPR-PTNLTFLHYWYKNSNDKQVQECGHYLFSEVTAGCWLQKEEIHLYETFFVQLR 133
QY 215 GSSEQPIRPSYFIFQLQNIKVPMPDYLSTLVKNSEINLKNMMPKGPPIPAKCFIYEIE 274
Db 134 DPRE--PRQSTOKLKLQNLVIPAPENLTNLHLSQSLWS---NRHLDHCLHEHVQ 188
QY 275 FTED-OTTWTTTVEINEIQITRSTNESQKL-CFLVRSKVNIYCSDDGIWSEWSDQWK 332
Db 189 YRSDWRDSWTEQSDVHRNSFSLPSVDGQKFTYTPRVSRYNPLCGSAQRWSEWSHPHWGS 248
QY 333 DIWKETLVF---FLIPAFVSIFVLVITCLLYKORAL 367
Db 249 NTSKENPLFASEAVLPLGSMGLIISLI-CVYWLERSI 286
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Db 46 CWEPGADGGLPTNTLYHKEGETLIHECPDY-KTGGPN-SCYFSKKHTSIWKMYVITV 103
Qy 214 N-----GSSESQIRPSYFIFQLQNIWKPMPPDYLSLTVKNSEE-----INLKNMP-RGP 263
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Db 104 NAINQMGISSDPL-----YVHTYVIVEPEPPANLTLELKHPEDRKPYLWIKWSPTMTD 158
| | | | : | | | | | | | | | | : | | | |
Qy 264 IPAKCFI--YEIEF-TEDGTTWVT--TTVENEIQITRTSNESQKLCFLVRSKVNIYCSDD 318
: : | | | | | | | | | | : : | | | | | | | |
Db 159 VKSGWFIIQYEIRLKEKATDMETHFTLKQTLKIFNL-YFQOKYLVQIRCK-----PDH 212
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Qy 319 GIWSEWSDEQCMK-----GDIWKETLVFFLIPFAFVSIEVL-----VITCLL 360
| | | | | | | | : | | | | | | | | : | | | |
Db 213 GIWSEWSPESSIQIPNDFPVKDTSMW-----IFVAILSAVICLIWVAVALKQYSMTCIL 268
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Search completed: September 20, 2002, 11:54:45
Job time: 144 sec

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OW nucleic - nucleic search, using sw model

Run on: September 23, 2002, 13:36:07 ; Search time 108.29 Seconds
(without alignments)
3298.099 Million cell updates/sec

Title: US-09-828-995B-60
Perfect score: 1454
Sequence: 1 ggcacagagctgagtttgtg.....aaangaaaaaaaaaaaaa 1454

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_patents_NA:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	842	57.9	1369	1	US-08-609-572-3
2	842	57.9	1369	4	US-08-841-751-3
3	842	57.9	1369	4	US-08-846-340-3
4	842	57.9	1369	4	US-08-846-344-3
5	727	50.0	1525	1	US-08-609-572-1
6	727	50.0	1525	4	US-08-841-751-1
7	727	50.0	1525	4	US-08-846-340-1
8	727	50.0	1525	4	US-08-846-344-1
c 9	42.2	2.9	7218	1	US-08-232-463-14
10	40	2.8	7400	1	US-08-261-663A-1
11	40	2.8	7400	5	PCT-US95-07754A-1
c 12	38.4	2.6	731	1	US-08-451-405A-2
13	38.4	2.6	3355	2	US-08-933-821-3
14	38.4	2.6	3355	3	US-08-960-507-3
15	38.4	2.6	3355	4	US-09-136-828-3
16	37.4	2.6	940	2	US-08-471-717-1
17	37.4	2.6	1241	1	US-07-593-657-6
18	37.4	2.6	1241	4	US-08-942-012B-3
c 19	37	2.5	663	4	US-08-998-416-191
c 20	37	2.5	854	4	US-08-998-416-534
c 21	37	2.5	860	4	US-08-998-416-287
22	37	2.5	1472	4	US-08-781-420-10
c 23	37	2.5	1472	4	US-08-781-420-12
24	37	2.5	1472	4	US-08-874-102-10
c 25	37	2.5	1472	4	US-08-874-102-12
26	37	2.5	1881	4	US-08-874-102-46
c 27	37	2.5	1881	4	US-08-874-102-48

28	36.4	2.5	789	6	5219739-8	Patent No. 5219739
29	36.2	2.5	1096	1	US-08-525-507-4	Sequence 4, Appli
30	36.2	2.5	1631	3	US-09-118-319-1	Sequence 1, Appli
31	36.2	2.5	3046	1	US-08-525-507-7	Sequence 7, Appli
32	36.2	2.5	4284	1	US-08-525-507-14	Sequence 14, Appli
33	36	2.5	3573	4	US-09-353-585-4	Sequence 4, Appli
c 34	35.4	2.4	2639	4	US-09-374-135-1	Sequence 1, Appli
35	35.4	2.4	3848	4	US-09-112-096-28	Sequence 28, Appli
36	35.4	2.4	5668	4	US-09-112-096-14	Sequence 14, Appli
37	35.4	2.4	51952	3	US-08-947-823-1	Sequence 1, Appli
38	35.2	2.4	4797	4	US-09-354-243B-25	Sequence 25, Appli
39	35.2	2.4	5836	4	US-09-233-086-2	Sequence 2, Appli
40	35	2.4	790	6	5194596-8	Patent No. 5194596
41	35	2.4	3138	1	US-07-867-106-4	Sequence 4, Appli
42	34.6	2.4	2081	4	US-08-235-836C-71	Sequence 71, Appli
43	34.4	2.4	1956	4	US-08-559-896B-1	Sequence 1, Appli
44	34.4	2.4	3126	2	US-08-477-396A-3	Sequence 3, Appli
45	34.2	2.4	518	1	US-08-485-284A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-609-572-3
; Sequence 3, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
US-08-609-572-3

Query Match		57.9%;	Score 842;	DB 1;	Length 1369;
Best Local Similarity		80.6%;	Pred. No. 1.3e-206;		
Matches 1038;		Conservative 0;	Mismatches 235;	Indels 15;	Gaps 4;
QY	150	gagtggaactcaaaagtattgaactttggagaagaatggttttcattcaattcatttggtatcg	209		
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QY	210	attcctctatccctgctgttgcacagcatttgct---ctatgctttccaaatgctga	266		
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Db	189	GATAAAAGTTAAACCTCCCTCAGGATTTTTCAGATAGTGGATCCGGATACTAGGTATCT	248		
QY	327	ctctttgcaatggcaacctccatttattccggataattttaagggaatgcacaaatgaata	386		
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QY	387	tgaattaaaaataccgaacattgatgtaaaactggagaaccattcattaccaagaatct	446		
Db	309	TGAACATAAATACCGAAACATTTGGTAGTGAACATGGAAGACCATCATTTACTAAGNATCT	368		
QY	447	acattacaagaatgggtttgatctttaacaagaatttgaagcaagaataaacacactct	506		
Db	369	ACATTTACAAAGATGGGTTTGTATCTTAAACAAGGCGATTTGAAGCAAGATACACACGCTTT	428		
QY	507	gcagcaccaatgcacaaatggatcgaagcttagaagttcatctgggcagaacactactattg	566		
Db	429	ACCATGGCAATGCACAAATGGATGGAAGTTCAAAGTTCTCTGGCAGAACTACTTTATTTG	488		
QY	567	gacatcaccacaagaagaaatcgggaaactaaaatcagaatattggactgtgtattattacaa	626		
Db	489	GATATCACCACACAGAAATCCAGAACTAAAGTTTCAGGATATGGATGGGTATATTACAA	548		
QY	627	ctggcaaatattagctgtctgtggaacctggcattgggtgtccatttttgataccaatta	686		
Db	549	TTGGCAATATTTACTCTGTCTTCTTGGAAACCTGGCATAGGTGTACTTCTTGTATACCAATTA	608		
QY	687	ccagtgctttactggtatgaggtttggaccattcagcagagtgactgattacataca	746		
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QY	807	tttctacatctgttaatcgggtcattcagaatccccagcctatacagaccagctattttat	866		
Db	729	TTTCTATATTTGTTTAAATGGATCATCAGAGAACAAAGCCTATCAGATCCAGTTATTTAC	788		
QY	867	tttccagctcaaaatatagtttaaacctatgcacagactacccttagcttactgtgaa	926		
Db	789	TTTTTCAGCTTCAAAATATAGTTTAAACCTTTGGCGGAGTCTATCTTTACTTTTACTCGGA	848		
QY	927	gaatccagaggaataataacctgaaatcggaactgacctaaagaccattccagccaaatcg	986		
Db	849	GAGTTTCATGTAATTAAGTCAATGGAGCATACCTTTGGGACCTATTTCCAGCAAGGTG	908		
QY	987	tttctattatgaattgaattcaacagagatggttactacttgggtgactaccacagttga	1046		
Db	909	TTTTTGATTATGAATTTGAGATCAGAGAGATGATACCTTTGGTGTGCTACAGTTTGA	968		
QY	1047	gaatgagatcacaaatcacaaagacataaataagagccaaatattgcttttttggtga	1106		
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QY	1284	actgaaacgat-----ctttcacaaaaaagaagctcttttctcatcaagacacat	1336
Db	1209	CCAAAAAATGATCCAGAAATTTTCTGTATACATGAAGACTTTCCATATCAAGAGACAT	1268
QY	1337	tctgttgactcagtaactttcagctcttatggccagatgtttaaatatgagctcttattaaac	1396
Db	1269	GGTATTGACTCAACAGCTTTCCAGTC--ATGGCCAAATGTTCAATATGAGTCTCAATAAAC	1326
QY	1397	tgaagcttttctcctaataattgaataaa	1424
Db	1327	TGAATTTTCTTTCGCGAAAAAATAAAAAA	1354

RESULT 2
US-08-841-751-3
; Sequence 3, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Mary
; APPLICANT: Filtz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
US-08-841-751-3

Db	1089	ATGCTGGGAAGGTAAGACCTATCGAAGAAACTTTGCTACGTTTCTGGCTACCATTTGG	1148
Qy	1224	tttgtctcaatatattgttttgtaataacttgcctgcttttggatataagcaagggtttt	1283
Db	1149	TTTCATCTTAATATTAGTTATATTGTAACCGGTCTGCTTTTTCGCTAAGCCAAACACCTA	1208
Qy	1284	actgaaaaacgat-----ctttcatacaaaaaagaagagctcttttctcatcaagaacacat	1336
Db	1209	CCCAAAATGATTCACGAATTTTCTGTGATACATGAAGACTTTCCATATCAAGAGACAT	1268
Qy	1337	tcgttgactcagtaactttcagctcttatggccagatgttaaatatgagctcttattaaac	1396
Db	1269	GGTATTGACTCACAGTTTCCAGTC--ATGGCCAAATGTTCAATATGAGTCTCAATTAAC	1326
Qy	1397	tgaagctttctcctaattgtaataaa	1424
Db	1327	TGAATTTTCTTCGAAAAAATAAA	1354
RESULT 3			
US-08-846-340-3			
; Sequence 3, Application US/08846340			
; Patent No. 6248714			
; GENERAL INFORMATION:			
; APPLICANT: Collins, Mary			
; APPLICANT: Donaldson, Debra			
; APPLICANT: Fitz, Lori			
; APPLICANT: Neben, Tamlyn			
; APPLICANT: Whitters, Matthew			
; APPLICANT: Wood, Clive			
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN			
; NUMBER OF SEQUENCES: 9			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Genetics Institute, Inc.			
; STREET: 87 Cambridgepark Drive			
; CITY: Cambridge			
; STATE: MA			
; COUNTRY: USA			
; ZIP: 02140			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/846,340			
; FILING DATE:			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/609,572			
; FILING DATE:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Brown, Scott A.			
; REGISTRATION NUMBER: 32,724			
; REFERENCE/DOCKET NUMBER: G15268			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (617) 498-8224			
; TELEFAX: (617) 876-5851			
; INFORMATION FOR SEQ ID NO: 3:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1369 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			
; MOLECULE TYPE: cDNA			
; HYPOTHETICAL: NO			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 103..1245			
; US-08-846-340-3			

Query Match	57.9%;	Score 842;	DB 4;	Length 1369;							
Best Local Similarity	80.6%;	Pred. No. 1.3e-206;									
Matches 1038;	Conservative	0;	Mismatches 235;	Indels 15; Gaps							
Qy	150	gagtggaactc	caaaagtatt	gaactctggaagaatg	gctcttcattcatttggtg	tgcgg	209				
Db	69	GAGAGGCAAT	ATCAAGGTTT	TAATCTCGGAGAAAT	GGCTTCGTTCGTTGGCGTAT	TCGG	128				
Qy	210	attcctctata	caccctgctgtt	gtgcacagcatt	ggct---ctatgctttcaaat	gctga	266				
Db	129	ATGCTTATAT	ACCTTTCAT	AAGCACAACAT	TTCGGCTGTACTTCATCT	TTCAGACACGA	188				
Qy	267	gataaagtt	taactcctcctc	agattttgagat	gtaggcacctggat	tatttaggtat	ct	326			
Db	189	GATAAAGTT	TAACCCCTC	CAGGATTTT	GAGATAGTGAT	CCGCGATAC	TTAGGTTATCT	248			
Qy	327	ctcttgcaat	ggcaacotcc	attatttccggata	aatlttaaggaatg	cacaataga	ta	386			
Db	249	CTATTTCGA	ATGGCAACCC	CCACTGCTCT	TGGATCATTTT	AAGGAATGC	ACAGTGAATA	308			
Qy	387	tgaattcaaat	accgaaacatt	gtagtga	aaactggaagaccat	cattaccaga	aatct	446			
Db	309	TGAACATAAA	TACCGAACA	CTTGGTAGTGA	AACATGGAAGAC	CATCATTACT	TAAGAAATCT	368			
Qy	447	acattcaaat	agatgggtt	gtgacttca	caaaagttattga	agcaaga	gataaaca	acttct	506		
Db	369	ACATTACAA	AGATGGCTT	TGATCTTAA	CAAGGCGATT	TCAAGCGA	GATACACACGCTTT	428			
Qy	507	gcagcac	aatgcacaaa	tgatcgat	cgagagttaga	agttcattgg	gcagaa	aaactact	ttg	566	
Db	429	ACCATGGCA	ATGCACAAAT	GGATCAGAAG	TCTCAAAGTTC	CTGGCGAC	AAACTACTTATG	488			
Qy	567	gacatc	ccacaag	gaatcgg	gaactaaa	attcagat	gatgact	gtgtata	tacaa	626	
Db	489	GATATCAC	CAAGGAAT	TCCAGAAAC	TAAAGTTCAG	GATATGGA	TGCGTATATTACAA	548			
Qy	627	ctggcaat	tatttagt	ctgctctgg	aaacctgg	catgggtgtcc	attttgat	acc	aat	686	
Db	549	TTGGCAAT	ATTTACTCT	GTCTTTGG	AAACCTGG	CATAGTCTACTTCT	TGTGATACCAATTA	608			
Qy	687	ccagtg	tctttact	cggtatag	gggttgg	acattcag	cagagtg	tactgat	tac	aa	746
Db	609	CAACTGT	TTTTACTGT	GTATGAG	GGCTTG	GATCATGCAT	TACAGTGTGT	TGATTACAT	CAA	668	
Qy	747	ggttaact	gga	aaaaat	atgggat	gcaggttcc	ctctattg	agatc	atca	ga	806
Db	669	GGCTGAT	GGCAAAAT	ATAGGAT	GCAGATTTCC	CTATTGG	AGGCATCAG	ACTATAA	GA	728	
Qy	807	ttctacat	ctgtgt	taattgggt	ctatc	agaa	tcc	cag	ctatc	ag	866
Db	729	TTTTCTAT	ATTGTTT	AATGGAT	CATCAG	AGAACG	CTATCAG	ATCCAG	TTATTT	CA	788
Qy	867	tttccag	cttcaaaa	tatagtt	taaac	ctatg	ccacc	gactac	ctt	ag	926
Db	789	TTTTTCAG	CTTCAAAAT	ATAGTTAA	ACCTTTG	CGCGAC	GTATCTTACT	TTTTT	TACTCG	GA	848
Qy	927	gaattc	ag	ggaatt	aaact	gaaatg	gaacatg	cc	taaa	ag	986
Db	849	GAGTTCAT	GTGAAAT	TAAAGCT	GAATGG	AGCATAC	CTTTGG	AGCCTAT	TTCCAG	CAAG	908
Qy	987	tttca	tttata	gaaatt	gaattc	acagag	gatggt	tact	actt	gggt	1046
Db	909	TTTTTGAT	TATGAAT	TGAGAT	CAGAG	AGATGAT	ACTACCT	TGGT	GACTG	CTACAG	968
Qy	1047	gaatg	atg	atata	caaat	caacat	caaat	gaa	agcc	aaat	1106
Db	969	AAATGAA	ACATAC	CCCTT	GAAAC</						

Query Match 57.9%; Score 842; DB 4; Length 1369;
Best Local Similarity 80.6%; Pred. No. 1.3e-236;
Matches 1038; Conservative 0; Mismatches 235; Indels 15; Gaps 4;

Qy 150 gagtggaactcaaaaglatigaaactctggaggaatgctcttcattcttctggtgagtcg 209
Db 69 GAGAGGCAATATCAAGGTTTAAATCTCGGAATAAGGCTTTCGTTGCTGGCTATCGG 128
Qy 210 attctctatccctgctgtgttcacagcatttggct---ctatgctttcaaaatgctga 266
Db 129 ATGCTTATATACCTTTCGTAAGACACAACTTTGGCTGACTTTCATCTTCAGACACCGA 188
Qy 267 gataaaagttaactctctcctcctggattttgagatagtggaacctgatatagtggtatct 326
Db 189 GATAAAAGTTAAACCTCTCCTCAGGATTTTCAGATAGTGGATCCCGGATACCTTAGGTTATCT 248
Qy 327 ctctttgcaatggaacctccattatttccggaataattttaagggaatcacaaatagaata 386
Db 249 CTATTTGCAATGGCAACCCCACTGCTCTGGATCATTTTAAGGAATGCACAGTGGAAATA 308
Qy 387 tgaattaaaaacccgaacattgatagtgaaactggagaccatcattaccagaatct 446
Db 309 TGAACATAAATACCGAACATTTGGTAGTGAACATGGAAGACCATCATTAAGAACT 368
Qy 447 acattacaagaatgggtttgatctttaacaaaggttatggaagcaagataaaacacacttct 506
Db 369 ACATTTACAAAGATGGTTTGTATCTTAAACAGGGCATTTGAAGCGAAGATACACACGCTTT 428
Qy 507 gccagcacaatgcaaaatgatcagaagttagaagttcattcagggcagaaactactatttg 566
Db 429 ACCATGGCAATGCACAAATGATCAGAAGTTCAAAGTTCCTGGCGAGAATCTATTATG 488
Qy 567 gacatcaccaagaagaaatcgggaaactaaaaattcaaatggaactgtgtattatacaa 626
Db 489 GATATCACCAAGGAATTCAGAAACTAAAGTTTCAGGATATGGATTGCGTATATTACAA 548
Qy 627 ctggcaattatttagctctctcttgaaacctggcaatgggttccatttttgataccaatta 686
Db 549 TTGCAATATTACTCTCTCTTGAAACCTGGCATAGGTGTACTTCTGTATACCAATTA 608
Qy 687 ccagtgcttactgtatgaggtctggaccattcagcagagtgactgtactgtatcatcaa 746
Db 609 CAACTGTTTACTGGTATGAGGGCTTGATCATGCATTCATGAGTGTGTGATTACATCAA 668
Qy 747 ggttaatgaaaaataatggatgcaggtttccctctatttggagtcatcagacataaaaga 806
Db 669 GCCTGATGCACAAATATAGGATGCAGATTCCCTATTTCGAGGCGATCAGACTATAAGA 728
Qy 807 ttctacatctgtgttaatgggtctacagaatcccgacctatcagaccagctattttat 866
Db 729 TTTCTATATTTGTGTTAATGGATCATCAGAGAAACAAGCCTATCAGATCGAGTTATTTAC 788
Qy 867 ttctcagctcaaaatagttaaacctatgccacagactaccttagtcttactgtgaa 926
Db 789 TTTTCAGCTTCAAAATATAGTTAAACCTTTGCGCGAGTCTATCTACTTTTACTTCGGGA 848
Qy 927 gaattcagaggaataaacctgaaatggaacatgccttaaaagaccattccagccaaatg 986
Db 849 GAGTTCATGTGAATTAAGCTGAATGGAGCATACCTTTGGGACCTATTCCAGCAAGGTG 908
Qy 987 ttctattatgaattgaattcacagagatgggttactacttgggtgactaccacagttga 1046
Db 909 TTTTGATTATGAATTTAGATCAGAGAAGATGATACCTTGGTGGTACTGCTACAGTTGA 968
Qy 1047 gaatgagatacaaaatcacagaacatcaaaatgaaagccaaataattatgcttttggtaag 1106
Db 969 AAATGAAACATACACCTTGAACAAACAAATGAAACCCGACAAATATGCTTTGTAGTAG 1028
Qy 1107 aagtaagtgaattatttctcagatgatggaatctggagtgagtgagtgagtaaca 1166
Db 1029 AAGCAAAAGTGATATTTATTTGCTCAGATGACCGAAATTTGGAGTGAGTGAGTGATAACA 1088
Qy 1167 atgctggaaggtga---catatggaaggaacaccttagtatttttcttgataccatttgc 1223

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Db 1149 TTTTCATCTTAATATAGTTATATTTGTAAACCGTCTGCTTTTTCGTAAGCCAAACACCTA 1208
Qy 1284 actgaaaaacgat-----cttctacaaaaaagaagctctttctcatcacaagacacat 1336
Db 1209 CCAAAAATGATTCAGAAATTTTCTGTGATACATGAAGACTTTCCATATCAAGAGACAT 1268
Qy 1337 tetgttgactcagtaaaccttcagttcttatggccagatgttaaatatgagctcttattaaac 1396
Db 1269 GGTATTGACTCAACAGTTTCCAGTC--ATGGCCAAATGTTCAATATGAGTCTCAATAAAC 1326
Qy 1397 tgaagcttttctcccaaatattgataaa 1424
Db 1327 TGAATTTTCTTGGCAAAAAA 1354

RESULT 5
US-08-609-572-1
; Sequence 1, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
US-08-609-572-1

Query Match 50.0%; Score 727; DB 1; Length 1525;
Best Local Similarity 72.5%; Pred. No. 3.7e-177;
Matches 1033; Conservative 0; Mismatches 361; Indels 30; Gaps 6;

QY 37 aggaagggagcttagagattcttaattaaatgtctccaaactgggaagagaaaaaaag 96
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QY 97 aggaactgtgataaattgacctatgataattcattctcttgagaacacatattattggtgga 156
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QY 217 tataccctctgtttgacagcatttggctctctatgcttctcaaaagtctgagataaaagt 276
Db 283 TGTTCATCTCTCTTTGTAACAATAACTAGGCTAT-----TCTTTGGAGATAAAGTT 333
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QY 397 taccgaacattgtagtgaactgggaagaccatttaccgaagaatctacattacaaa 456
Db 454 TACCGAAATGTTGATAGCCACAGCTGGAAGACTATAAATTTACTAGGAATCTAATTTACAG 513
QY 457 gatgggttgattcttaacaaaggtattgagcaaaagataaaacacactcttgcagacaaa 516
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QY 517 tgcacaaatggatcgaaacttgaagtctcatgggcagaacacttatttggacatcacca 576
Db 574 TGTACAAATGGATCAGAACTCAAAAGTCCATGGATAGAAGCTTCTTATGGGATATCAGAT 633
QY 577 caaggaaatcgggaaactaaaatccaagatatggactgtgtattacaaactggcaaat 636
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QY 637 ttagtctcttgaaacctggcctgagtggtgtccatttttgatcaccaattaccagttgttt 696
Db 694 TTGGTCTGTCTTGGAAACCTGGCAGACAGTATATTCTGTACCAACTATACCATGTTT 753
QY 697 tactggtatgagggcttggaaccattcagcagagtactgattacatacgaagttaatgga 756
Db 754 TTCTGTATGAGGGCTTGGATCATGCTTTACAGTGTGCTGTATACCTCCAGCATGATGAA 813
QY 757 aaaaatatgggtgcaggtttccctatttggagtcacagactataaaagatttctacatc 816
Db 814 AAAAAATGTTGGATGCAAACTGCAAACTTGGACTCATCATCAGACTATAAAGATTTTTTATC 873
QY 817 tgtgtaaatgggtatcatcagaatccagacctatacagaccagactatttttttccagctt 876
Db 874 TGTGTTAATGGGATCTTCAAAGTTGGAACCCATCAGATCCAGCTATACAGTTTTTCAACTT 933
QY 877 caaaatatagtttaaacctatgccaccagactaccttagtcttactgtgagaattcagag 936
Db 934 CAAAATATAGTTAAACCATTTGCCACCAGAAATTCCTTCATATTAGTGTGGAGAAATTCATTT 993
QY 937 gaaattaaactgaaattggaacatgctaagaaggaccattccagcccaaatgttttctattat 996
Db 994 GATATTAGAATGAAATGGAGCACACCTGGAGGACCCATTCACCAAGGTTTACACTTAT 1053
QY 997 gaaattgaattcacagagatggtactacttgggtgactacacagattgagaatgagata 1056
Db 1054 GAAATGTGATCCGAGAACACATATTTCTCTGGAGTCTGCCACACAGAAAAACCATATG 1113
QY 1057 caaatcacagaacatcaaatgaaagcccaaaaattatgcttttttggtaagaagtaagtg 1116
Db 1114 AAGTTGAAGGAGAGCAAAATGAAGTGAAGACCTATGCTTTTGTGAAGATGAAGGTC 1173

QY 1117 aatattattgtccagatgatgaatctgagtgagtgagtgatgaacaatgctgaaa 1176
Db 1174 ATATATATATTGTGCAGATGATGGAATTTGGAGGAATTTGGAGGAATTTGGGAA 1233
QY 1177 ggtgacatggaaggaacaccttagtattttcttctgataccatttcttcttctcaata 1236
Db 1234 GGTTCACACAGGGCCAGACTCAAAAGATTATTTCATAGTACCAGTTGTCTTTCTTTATA 1293
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Db 1414 AATTTCTTGACATAGAGCCAG----CCAGCAGAGTCATATTAAACTCAA-TTTCCTCTTA 1468
QY 1411 aaatattgataaatacttatttttaaaangaaaaaataaaaaa 1454
Db 1469 AATTTGGAATACATCTTCTTGAAATCCAAAAAATAAAAAA 1512

RESULT 6

US-08-841-751-1
; Sequence 1, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:

NAME/KEY: CDS
LOCATION: 256...1404
us-08-841-751-1

Query Match 50.0%; Score 727; DB 4; Length 1525;
Best Local Similarity 72.5%; Pred. No. 3.7e-177; Indels 30; Gaps 6;
Matches 1033; Conservative 0; Mismatches 361;

Qy 37 aggaaggaagctcttagagattcctaataatgctcccaactggagaagagaaaaaag 96
Db 113 AGGAGGAAACACGTAGAGATTCAATTAGTCTCT- ---AATGTGAAAGGAGACAAAG 168
Qy 97 aggaacctgataaattgacctatgataaattcatttcttgagaaaccatattattgagtga 156
Db 169 AGGTCTTGATTAACCTGCTGTGATAATACATATTTCTTGAGAAACCATATTATTGAGTAGA 228
Qy 157 aacttcaaatgattgaactcttgaggaaatggctttcattcatttgagatgcgattctctc 216
Db 229 GCTTTTCAGCACACTAAATCCTGGAGAAATGGCTTT- ----TGTGCATATACAGATGCTTG 282
Qy 217 tataacctgctgtttgacagcatttggctctctatgctttcacaatgctgagataaaagt 276
Db 283 TGTTCATCTCTTTGTACATACTACTGGCTAT- -----TCTTTGGAGATAAAGTT 333
Qy 277 aatcctctcaggattttgagatagtgaccctggatatttaggttatctctctttgcaa 336
Db 334 AATCCTCCTCAGGATTTTGAATAATTGGATCCTGGATTACTTGGTTATCTCTATTTTGCAA 393
Qy 337 tggcaacctccaattattcccgataaattttaagggaatgcacaatagaatagaataaaa 396
Db 394 TGGAAACCTCTGTGGTTTATAGAAAATTTTAAAGGCTGTACACTAGATATAGTATAAAA 453
Qy 397 taccgaacattgtagtgaacactggagaccatcatcaccagaatctacattacacaa 456
Db 454 TACCGAATGTGTAGCGCAGCTGGAGACTATAAATTACTAGGAATCTAATTATTACAAAG 513
Qy 457 gatgggtttgatcttaacaaagggtatgaagcaaaagataaaacacactcttgcgcagcaaa 516
Db 514 GATGGTTTGTATCTTAATAAGGCATTGAAGGAAAGATACGTAACGTCATTGTGTCAGAGCAT 573
Qy 517 tgcacaaatgatacagaagttagaagttcatgggcagaaactacttatggacatcacca 576
Db 574 TGTACAAATGGATCAGAAAGTACAAAGTCCATGGATAGAAAGCTTCTTATGGGATATCAGAT 633
Qy 577 caagaaatcggaactaaactaaatcaagataggaactgtgtatatatacaactggcaaat 636
Db 634 GAAGGAAGTTTGGAAACATAAAATTCAGGACATGAAGTGTATATATTATAACTGGCAGTAT 693
Qy 637 ttagtctctcttggaaacctgcatgggtgtccatttttgataccaaattaccagttgttt 696
Db 694 TTGGTCTGCTCTTGGAAACCTGGCAAGACAGATATATTCTGATACCAACTATACCATGTTT 753
Qy 697 tactggtatgagggccttgaccattcagcagagtgtaactgattacatcaaggttaagtga 756
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Db 814 AAAAATGTTGGATGCAAACTGTCCAACTTGGACTCATCAGACTATAAAGATTTTTTATTC 873
Qy 817 tgtgtaattgggtcatcagaatccccagcctatccagaccagctattttattttcagctt 876
Db 874 TGTGTTAATGGATCTTCAAAGTTGGAACCCATCAAGTCCAGCTATACAGTTTTTCAACTT 933
Qy 877 caaaatatagttaaacctatgcccacagactacccttagtcttactgtgaagaattcagag 936
Db 934 CAAAATATAGTTAAACCATTTGCCACCAAGAAATTCCTTTCATATTAGTGTGGAGAAATCCCAT 993
Qy 937 gaaattaacctgaatgaagaaatgcttaagagaccattccagccaaatgtttctatttat 996
Db 994 GATATTGAATGAATGGAGCACACCTGGAGACCCATTCACCAAGGTGTACACTTAT 1053

Qy 997 gaattgaattcacagagagatgggtactactcttgggtgactaccacagttgagaatagata 1056
Db 1054 GAAATTTGTATCCGAGAGACGATATTTCTGGGAGTCTGCCACACACAAAAACGATATG 1113
Qy 1057 caaatcacagaacacaaatgaagccaaataatctcttttggtaagaagtaaaagt 1116
Db 1114 AAGTTGAGAGAGAGAGACAAATGAAAGTGAAGACCTATGCTTTTGTAAAGATGTAAAGTTC 1173
Qy 1117 aatatttattgtcagatgaggaatctgtgagtgagtgagtgatgaacaaatgctggaaa 1176
Db 1174 AATATATATTGTGCAGATGATGGAATTTGGAGCGAATGAGTGAAGAGCAATGTTGGGAA 1233
Qy 1177 ggtgcacatgagaagaaacetttagtatttttcttgataccattttgtcttctcacaata 1236
Db 1234 GGTTCACAGGGCCAGACTCAAAAGATTATTTTCATAGTACCAGTTTGTCTTTCTTTATA 1293
Qy 1237 ttgttttggtaataaacttgctgctttgttataagcaaggcctttactgaaacgac 1296
Db 1294 TTCTTTTGTACTTCTTTTGCCCTTATTGTGGAGAGGAAGAACCTGAAACCCACATTTGAGC 1353
Qy 1297 ttctc-----atacaaaaaaagaagtcttttctctcaacagacacattctgttgactcagt 1350
Db 1354 CTCCATGTGGATCTGAACAAAGAGTGTGCTGTATGAAGATACCTCTGTATAACACC 1413
Qy 1351 aacttctcagttctatggccagatgttaaataatgactcttattataaactgaagctttctc 1410
Db 1414 AATTTCTTGACATAGAGCCAG- ---CCAGCAGGAGTGCATATTAAACTCAA-TTTCTCTTA 1468
Qy 1411 aaatatgaataaaacttattttaaaangaaaaaataaaaaa 1454
Db 1469 AAATTCGAATACATCTTCTTGTAAAATCCAAAAAATAAAAAA 1512

RESULT 7
US-08-846-340-1
; Sequence 1, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
US-08-846-340-1

Query Match          50.0%; Score 727; DB 4; Length 1525;
Best Local Similarity 72.5%; Pred. No. 3.7e-177;
Matches 1033; Conservative 0; Mismatches 361; Indels 30; Gaps 6;

QY 37 aggaaggggaagcttagagatcttaataatgtctccaaactggagaagagaaaaaag 96
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QY 97 aggaactgtgataaattgacctatgataattcattctcttgagaacacattatttgagtga 156
DB 169 AGGTCTGTGTGAACCTGCTGTGAATAACATTTCTTGAGAAACCATATATTGAGTAGA 228

QY 157 aacttcaaaagtattgaattcttgaggaaatggctttcattcatttgatgctggattccctc 216
DB 229 GCTTTTCAGCACACTAAATCCTGGAGAAATGGCTTT-----TGTGCATATCAGATCCTTG 282

QY 217 tataccctcctgtgttgagcagcattggctctctatgcttccaatgctgagataaaagt 276
DB 283 TGTTCCTTCTTTTGTGTAACAATAAGTGGCTAT-----TCTTTGGAGATAAAAGTT 333

QY 277 aatccctccagattttgagatagtgagccctggatatttaggttatctctctttgcaa 336
DB 334 AATCCTCCCTCAGGATTTTGAAATATTGGATCCTGGATTACTTGGTTATCTCTATTGCAA 393

QY 337 tgggaacctccattttccggataatttttaagggaatgcacaaatagaaatgaaattcaaaa 396
DB 394 TGGAAACCTCCTGTGTTATAGAAAAATTTAAGGGCTGTACACTAGAAATATGAGTTAAA 453

QY 397 taccgaacacatgtagtgaaacactggagaccatcattaccagaagaattacattacaaa 456
DB 454 TACCGAAATGTTGATAGCCACAGCTGGAAGACTATAAATTTACTAGGAATCTAATTTACAAG 513

QY 457 gatgggttgatcttaacaaagttattgaagcaagataaacaacactctctgcagacaaa 516
DB 514 GATGGGTTTGATCTTAATAAAGGCATTGGAAGGAAGATACGTACCGATTTTGTGAGAGCAT 573

QY 517 tgcaacaaatgggatcagaagttagaagttcatgggcagaaactactatttggacatcacca 576
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QY 637 ctgactcctctgaaacctggcagtggtgtccatttggataccaattaccagttgttt 696
DB 694 TTGGTCTGCTCTTGGAAACCTGGCAAGACAGTATATTCTGTACCAACTATATACCATGTTT 753

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DB 754 TTTCTGATGAGGGCTTGGATCATGCTTACAGTGTGCTGATTAACCTCCAGCATGATGAA 813

QY 757 aaaaaatgggtgagcaggtttccctatttggagtcacatcagacataaagatttctacatc 816
DB 814 AAAAAATGTTGGATGCAAACTGCCAACTGGGACTCATCAGACTATAAAGATTTTTTATC 873

QY 817 tgtgtaaatgggtcatcagaatcccgactatcagaccagctattttttttcagctt 876
DB 874 TGTGTTAATGGATCTTCAAGTTTGGAAACCCATCAGATCCAGCTATACAGTTTTCAACTT 933
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QY 877 caaaatatagtttaaaccttatgcaccagactaaccttagtcttactgtggaattcagag 936
DB 934 CAAAATATAGTTAAACCATTTGCCACCAGAAATTCCTTCATATTAGTGTGGAGAAATTCATT 993

QY 937 gaaattaacctgaaatggacatgacctaaagagaccattccagccaaatgtttcatttat 996
DB 994 GATATTAGAATGAAATGGAGCACACCTGTGAGGACCCATCCACCAAGGTGTTACACTTAT 1053

QY 997 gaaattgaattcacagagagatggtactacttgggtgactaccacagattgagaaatgagata 1056
DB 1054 GAAATTTGTGTCGGAAGACGATATTTCTCTGGAGTCTGCCACAGACAAAACGATATG 1113

QY 1057 caaatcacagaacatcaaatgaaagccaaataattatgcttttggtaagaagataaagt 1116
DB 1114 AAGTTCAAGAGGAGAGACAAATGAAAGTGAAGACCTATGCTTTTGTGAAGATGAAGGTC 1173

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QY 1237 ttgtttgtgtaataactgtcctgtttgtataagcaaaagggcttactgaaaacgac 1296
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QY 1351 aacttccagtcttatggccagatgttaaatatgactcttattaaactgaagcttttctc 1410
DB 1414 AATTTCTTGACATAGAGCCAG---CCAGCAGGAGTCATATAAAGCTCAA-TTTCCTCTTA 1468

QY 1411 aaatattgataaaacttattttaaaangaaaaaataaaaaa 1454
DB 1469 AAATTTGGAATACATCTTCTTGAAATCCAAAAAATAAAAAA 1512

RESULT 8
US-08-846-344-1
; Sequence 1, Application US/08846344
; Patent No. 6268480
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,344
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
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; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
US-08-846-344-1

Query Match          50.0%; Score 727; DB 4; Length 1525;
Best Local Similarity 72.5%; Pred. No. 3.7e-177;
Matches 1033; Conservative 0; Mismatches 361; Indels 30; Gaps 6;

Qy 37 aggaaggaaagctcttagagattctaataatgtctccaaactgggagagagaaaaaaag 96
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Qy 97 aggaacctgataattgctctgataaattcatttcttgagaaaccattatttagtgga 156
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Qy 157 aactcaaaagtatgaactctgggaatgctttcattcatttggatgctcgattccctc 216
Db 229 GCTTTACGACACATAATTCCTGGAGAAATGGCTTT-----TGTCATATCAGATGCTTG 282

Qy 217 tataccctctgtttgacagcatttggctctatgctttcaaatgctgagataaaagt 276
Db 283 TGTTCATTCTCTTTGTACAAATAACTGGCTAT-----TCCTTGAGATAAAAGTT 333

Qy 277 aatcctctcaggattttgagatgagagaccctggatatttaggtatctctcttgcaa 336
Db 334 AATCCTCTCAGGATTTTGAATAATATGGATCTGGATTACTTGGTTATCTCTATTATTGCAA 393

Qy 337 tggcaacctccattatttccggataattttaagaatacacaaatagataatgaattaaa 396
Db 394 TGGAAACCTCTGTGGTTATAGAAAATTTAAGGCGCTACACTAGATAATGAGTTAAA 453

Qy 397 taccgaaacattagtagtaaaactggagaccatcattaccaagaatctacattacaaa 456
Db 454 TACCGAAATGTTGATAGCGACAGCTGGAAGACTATAATTACTAGGAATCTAATTTACAAG 513

Qy 457 gatgggttgatcttaacaaaggattttaagaacaaagataaacacactctcgtccagacaa 516
Db 514 GATGGGTTTGATCTTAATAAAGGCAATTAAGGAAAGATACGTACGCATTTTGTTCAGAGCAT 573

Qy 517 tgcacaaatgatcagaagttcagaagttcagggagaaactacttattgacatcacca 576
Db 574 TGTCAAAATGGATCAGAAGTACAAGTCCATGGATAGAGGCTCTTATGGGATATCAGAT 633

Qy 577 caaggaaatcgggaaactaaataatcaagatatggactgtgtattaccaactggcgaat 636
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Qy 637 ttactctctcttgaaacctggcatgggtgtccattttgataccaattacagttgttt 696
Db 694 TTGGTCTGCTCTTGAAACCTGGCAAGACAGATATATTCTGATACCAACTATACCATGTT 753

Qy 697 tactggtatgaggcttggaaccattcagcagagtgctgattacatcaaggttaatgga 756
Db 754 TTCTGGTATGAGGCTTGATCATGCCCTACAGTGTGCTGATTACCTCCAGCATGATA 813
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Qy 817 tgtgttaatgggtcagcaaatcccagcctatcagaaccagctattttttcagctt 876
Db 874 TGTGTTAATGGATCTTCAAAGTTGGAACCCATCAGATCCAGCTATACAGTTTTTCAACTT 933

Qy 877 caaaatagtttaaaccttatgccaccagactaccttagcttactctgtgagaattccagag 936
Db 934 CAAAATATAGTTAAACCATTTGCCACCAGAAATTCCTTCATATTAGTGTGAGAAATTCAT 993

Qy 937 gaaattaaacctgaaatggaacatgcttaagagaccattccagccaaaatgtttctattat 996
Db 994 GATATTAGAAATGGAATGGAGCACACCTGGAGGACCCATTCACCAAGGTGTGTACACTTAT 1053

Qy 997 gaaattgaattcacagagagtggtactacttgggtgactaccacagtgtagaatgagata 1056
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Qy 1057 caaatcacagaacatcaaatgaaagccaaaattatgcttttggtaagaagtaaaagt 1116
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Db 1174 AATATATATTGTGCAGATGATGGAATTTGGAGCAATGGAGTGAAGAGGAATGTTGGGAA 1233

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Db 1234 GGTACACAGGCGCCAGACTCAAAAGATTTTTCATAGTACCAGTTTGTCTTTTCTTTATA 1293

Qy 1237 ttgttttggtaataaacttgcctgtcttctgtataagcaaaaggcttactgaaaacgacc 1296
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Qy 1297 tttc-----atacaaaaaaagaagcttttctcatcaagacacacattctgttgactcagt 1350
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Qy 1351 aacttctagctctttagccagatgttaaatatgactcttattaaactgaagcttttctctc 1410
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Qy 1411 aaattgaataaattcttattttaaaangaaaaaiaaaaaa 1454
Db 1469 AAATTTCCAAATACATCTTCTTGAANAATCCAAAAAIAAAAAAAAAA 1512
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RESULT 9
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
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US-08-232-463-14

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Best Local Similarity 2.7%; Pred. No. 0.17;
Matches 8; Conservative 171; Mismatches 114; Indels 0; Gaps 0;

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QY 963 taaagagaccattccagccaaatgtttcattatgaaattgaattcacagagatggtac 1022
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Db 1389 RRRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNR 1330

QY 1023 tacttgggtgactaccacagttgagaatgagatgatacaaatcacaagaacatcaaatgaaag 1082
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QY 1083 ccaaaaaattatgcttttggtaagaagtaagtaaatatttttctcagatgaggaat 1142
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Db 1269 RRRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNRNR 1210

QY 1143 ctggagtgagtgagtgagtaacaatgctggaaggtagacatatggaagaaa 1195
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RESULT 10
US-08-261-663A-1
; Sequence 1, Application US/08261663A
; Patent No. 5571706
; GENERAL INFORMATION:
; APPLICANT: Baker, Barbara J
; APPLICANT: Whitham, Steven A
; TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Margaret A. Connor, USDA-ARS
; STREET: 800 Buchanan Street
; CITY: Albany
; STATE: CA
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/261,663A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Connor, Margaret A
; REGISTRATION NUMBER: 30043
; REFERENCE/DOCKET NUMBER: 0094.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 559-6067
; TELEFAX: (510) 559-5777
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana glutinosa
; TISSUE TYPE: leaf
; FEATURE:
; NAME/KEY: exon
; LOCATION: Join(294..772, 1003..2098, 2941..3213, 5032..6600,
; LOCATION: 6934..6951)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 773..1002
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; LOCATION: 6934..6951)
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US-08-261-663A-1

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QY 969 accattccagccaaatgtttcattatgaaattgaattcacagagatggtactacttg 1028
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Db 2455 ATTCATTCACCTTTACCATTTATTTTATATAAAGTTACAAATTTATTGGTACTGTTTC 2514

QY 1029 ggtgactaccacagttgagaatgagatgatacaaatcacaagaacatcaaatgaaagccaaa 1088
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Db 2515 AGTTACAATTACTTTCCACATGGAAAACTTATAAATGGACTCCCAATAAATTAATAAGA 2574

QY 1089 attatgcttttggtaagaagtaagtaaatatttttctcagatgaggaatcgtggag 1148
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
4464.383 Million cell updates/sec

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Perfect score: 1454
Sequence: 1 ggcacgagctgagttgtg.....aaangaaaaaaaaaaaaa 1454

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1453	99.9	1454	22	AAS59962 Canine interleukin
c 2	1453	99.9	1454	22	AAS59963 Canine interleukin
3	1158	79.6	1158	22	AAS59964 Canine interleukin
c 4	1158	79.6	1158	22	AAS59965 Canine interleukin
5	1095	75.3	1095	22	AAS59966 Canine interleukin
c 6	1095	75.3	1095	22	AAS59967 Canine interleukin
7	947.8	65.2	954	22	AAS59968 Canine IL-13R extr
c 8	947.8	65.2	954	22	AAS59969 Canine IL-13R extr
9	947.8	65.2	1686	22	AAS59970 Canine IL-13R/IgG-

c 10	947.8	65.2	1686	22	AAS59971 Canine IL-13Ralpha
c 11	947.8	65.2	1686	22	AAS59976 Canine IL-13R/IgG-
c 12	947.8	65.2	1686	22	AAS59977 Canine IL-13Ralpha
c 13	947.8	65.2	1692	22	AAS59974 Canine IL-13R/IgG-
c 14	947.8	65.2	1692	22	AAS59975 Canine IL-13Ralpha
c 15	947.8	65.2	1698	22	AAS59972 Canine IL-13R/IgG-
c 16	947.8	65.2	1698	22	AAS59973 Canine IL-13Ralpha
c 17	877	60.3	878	22	AAS59960 Canine interleukin
c 18	877	60.3	878	22	AAS59961 Canine interleukin
c 19	842.4	57.9	1298	18	AAT86464 Human interleukin-
20	842.4	57.9	1298	18	AAT86464 Human interleukin-
21	842	57.9	1369	18	AAT95214 Nucleotide sequenc
22	842	57.9	1369	21	CDNA encoding the
23	842	57.9	1369	22	CDNA encoding IL-1
c 24	842	57.9	1369	22	AAS59991 Human interleukin-
c 25	842	57.9	1369	22	AAS59993 Human interleukin-
26	842	57.9	1369	22	AAD02335 Human interleukin
27	839.6	57.7	1288	19	AAC81416 Human IL-13 recept
28	839.6	57.7	1288	19	Human HR-1 recepto
29	839.6	57.7	1288	19	Human cytokine/pep
30	839	57.7	1289	18	Homo sapiens cDNA
31	787.4	54.2	1126	18	Human zcytor2 cyto
32	780.4	53.7	1167	18	Celebus maceque Zc
33	727	50.0	1525	18	Human zcytor2 cyto
34	727	50.0	1525	21	CDNA encoding the
c 35	727	50.0	1525	22	CDNA encoding IL-1
c 36	727	50.0	1525	22	AAS59990 Mouse Interleukin-
c 37	727	50.0	1525	22	AAS59992 Mouse Interleukin-
38	727	50.0	1525	22	Murine interleukin
39	712.6	49.0	951	24	Mouse IL-13 recept
40	712.4	49.0	947	19	Human soluble cyto
41	712.4	49.0	1079	19	Mature interleukin
42	620	42.6	620	22	Construct containi
c 43	620	42.6	620	22	Canine interleukin
c 44	419.4	28.8	1539	18	Canine interleukin
45	308	21.2	456	20	Human interleukin- EST clone CS520.

ALIGNMENTS

RESULT 1

AAS59962

ID AAS59962 standard; cDNA; 1454 BP.

XX

XX

AC AAS59962,

DT 29-JAN-2002 (first entry)

XX Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1454.

DE

XX Dog: interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;

KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;

KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;

KW immune response.

XX Canis familiaris.

OS

XX WO200177332-A2.

PD

XX 18-OCT-2001.

XX

PF 09-APR-2001; 2001WO-US11498.

XX

PR 07-APR-2000; 2000US-195659P.

PR 07-APR-2000; 2000US-195874P.

XX (HESK-) HESKA CORP.

PA

XX McCall CA, Tang L;

PI

XX WPI; 2001-657172/75.

XX

DR P-PSDB; AAU69135.

DR

Novel isolated canine protein, preferably canine immunoglobulin G protein or canine interleukin-13 receptor protein useful for regulating immune response of an animal and for developing regulatory compounds -

Claim 19: Page 173-175; 221pp; English.

The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13 proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence encodes a protein of the invention.

Sequence 1454 BP: 491 A; 238 C; 282 G; 442 T; 1 other;

Query Match 99.9%; Score 1453; DB 22; Length 1454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 aattaatgtctccaaactggagaagagaaaaaagagacctgtgataatggcctatga 120
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QY 121 taattcattcttgagaacacattattatgagtggaacttcaaaacttgaattcttga 180
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QY 181 ggaatggcttctcattcattgagtcggatctcctctatcacctgcttttgacagca 240
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QY 241 ttggctctatgctttccaaactgctgagataaaagttaactcctcctcagatttgagata 300
Db 241 ttggctctatgctttccaaactgctgagataaaagttaactcctcctcagatttgagata 300

QY 301 gtggacccctggattatgagttatctctctgtgcaatggcaacctccattatccggat 360
Db 301 gtggacccctggattatgagttatctctctgtgcaatggcaacctccattatccggat 360

QY 361 aatttcaaggaatgcacataagataatgataaaataccgaaacattgattgaaaaac 420
Db 361 aatttcaaggaatgcacataagataatgataaaataccgaaacattgattgaaaaac 420

QY 421 tggagaaccatcattaccagaatctacattcaaaagatgggtttgattcttaacaaagt 480
Db 421 tggagaaccatcattaccagaatctacattcaaaagatgggtttgattcttaacaaagt 480

QY 481 attgaagcaagaataaacaacattctgcccagacacaaatgcacaaatggatcagaagttaga 540
Db 481 attgaagcaagaataaacaacattctgcccagacacaaatgcacaaatggatcagaagttaga 540

QY 541 agttcatgggcagaactacttattggacatcacacagaaggaatcggaataaataatt 600
Db 541 agttcatgggcagaactacttattggacatcacacagaaggaatcggaataaataatt 600

QY 601 caagaatgagctgtgataattacaactggcgaatttttagtctgctcttgaaacctgpc 660
Db 601 caagaatgagctgtgataattacaactggcgaatttttagtctgctcttgaaacctgpc 660

QY 661 atgggtgtccatttgataccacattaccagttgttttactggtatgagggcttgacacat 720

Db 661 atgggtgtccatttgataccacattaccagttgttttactggtatgagggcttgacacat 720
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QY 781 tatttggagtcacagactataaagatttctacatctgtttaaagggttcacagaatcc 840
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RESULT 2
AAS59963/c
ID AAS59963 standard; cDNA; 1454 BP.
XX
AC AAS59963;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1454 complement.
XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX immune response.
OS Canis familiaris.
XX

PN WO200177332-A2.
XX 18-OCT-2001.
XX 09-APR-2001; 2001WO-US11498.
XX 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX (HESK-) HESKA CORP.
XX McCall CA, Tang L;
PI WPI; 2001-657172/75.
DR Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX Claim 19; Page 177-178; 221pp; English.
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins are useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13/alpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13 mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX Sequence 1454 BP; 442 A; 282 C; 238 G; 491 T; 1 other;
SQ
Query Match 99.9%; Score 1453; DB 22; Length 1454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 aattaatgtctccaaactggagaagagaaaaaagagaccctgtgataattgcctatga 120
Db 1394 AATTAATGCTCTCCAACTGGAGAAGAGAAAAAAGAGAGACCTGTGATAATTGCGCTATGA 1335
Qy 121 taattcattcttgagaaccatattattgagtgaaacttcaaatgagttggaatcttggga 180
Db 1334 TAATTCATTCTTGAGAACCAATATATTGAGTGAACCTTCAAGATATTGAATCTTGA 1275
Qy 181 ggaatgggtttcattcatttgatgcggattccctctatcacccctgttggtcacagca 240
Db 1274 GGAATGGCTTTCATTCTTGGATCGGATTCCTCTATACCTGCTTGTTCACAGCA 1215
Qy 241 ttggctctatgctttcaaatgctgagataaaagtaaatccctccctcagagattttgagata 300
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Qy 361 aattttaagggaatgcacataagaatatgaattaaataaccgaaacattgattgaaac 420
Db 1094 AATTTTAAGGAATGCACAAATAGAATATGAATTAATACCGAAACATTGATAGTGAAC 1035
Qy 421 tggagagccatcattaccagaagatcatcattacaagatgggtttgatctttaacaaagt 480
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Qy 481 attgaagcaagaataaaacacactcttcgcagcaccaatgcacaaatggatcagaagttaga 540
Db 974 ATTGAAGCAAGATAAACACACTTCTGCCAGCACCAATGCACAAATGGATCAGAAGTTAGA 915
Qy 541 agttcatggcgagaactacttatttggacatccaccacaaggaaatcgggaaactaaaaatt 600
Db 914 AGTTTCATGGCAGAAACTACTTTATTGGACATCCACACAGGAATAATCGGGAACATAAAT 855
Qy 601 caagatatggactgtgtatattacaactggcaatatttagtctgtctcttggaaacctggc 560
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Qy 721 tcagcagagtgactgattacatcaagggttaataagaaaaataatgggagtcgagggtttccc 780
Db 734 TCAGCAGAGTGACTGATTACATCAAGGTTAATGGAAAAAATATGGGATCGCAGGTTTCC 675
Qy 781 tatttggagtcacagactataaagatttctacatctgtttaatgggttcacagaatccc 840
Db 674 TATTTGGAGTCTACAGACTTATAAGATTTCATCTCTGTGTTAATGGGTTCATCAGAATCC 615
Qy 841 caqcctatcagaccagctatttatttccagctcctcaaatatagtttaaacctatgccca 900
Db 614 CAGCCTATCAGACCCAGCTATTTTATTTTCAGCTTCAAAATATATGTTAAACCTATGCCA 555
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Db 494 CCTAAAGGACCCATTTCCAGCCAAATGTTTCATTTATGAAATTTGAAATTCACAGAGATGT 435
Qy 1021 actacttgggtgactaccacagttgagaatgagatcacaaatcacagaacatcacaatgaa 1080
Db 434 ACTACTTGGGTGACTACCACAGTTGAGAATGAGATACAAATCACAAGAACATCAATGAA 375
Qy 1081 agccaaaaattatgcttttggglaagaagtaaaagtgaattatttattgctcagatgatgga 1140
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Qy 1141 atctggagtgagtgagtgatgaacaaactggaagagtgacatatgggaaggaacacctta 1200
Db 314 ATCTGGAGTGAGTGAGTGATGAACAATGCTGGAAGGTGACATATGGAAGGAAACCTTA 255
Qy 1201 gtattttcttggataccatttcttcttctcaatatttggtaataaacttgcctg 1260
Db 254 GTATTTTCTTCATACCATTTGCTTTGCTCAATATTTGTTGTAATAACTTGCCTG 195
Qy 1261 ctttggtaagaagaaggcttactgaaaaatcttctcaatacaaaaaaagaagctctt 1320
Db 194 CTTTGTATAGCAAGAGGCTTTACTGAAAAGCATCTTTTCATACAAAAAAGAAAGTCTTT 135
Qy 1321 tctcatcaagacacattctgttgactcaatcttctcagttcagtttggccagatgttaaat 1380
Db 134 TCTCATCAAGACACATCTCTGTGACTCAGTAACCTTCAGTCTTATGGCCAGAGTGTAAAT 75
Qy 1381 atgagttcttattcaactgaagcttttccctcaaatatttgaataaacttattttaaaaanga 1440
Db 74 ATGAGTCTTATTAACTGAAGCTTTTCTCAATATTGAAATTAATTAATTTAAAAANGA 15
Qy 1441 aaaaaaaaaaaaaa 1454
Db 14 AAAAAAAAAAAAAA 1
RESULT 3
AAS59964

DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1158 complement.
 XX
 KW Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.
 XX
 OS Canis familiaris.
 PN WO200177332-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 09-APR-2001; 2001WO-US11498.
 XX
 PR 07-APR-2000; 2000US-195659P.
 PR 07-APR-2000; 2000US-195874P.
 XX
 PA (HESK-) HESKA CORP.
 XX
 XX McCall CA, Tang L;
 PI
 XX
 DR WPI; 2001-657172/75.
 XX
 XX Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -
 PT
 XX
 PS Claim 19; Page 179; 221pp; English.
 XX
 CC The invention concerns an isolated canine protein, preferably canine
 CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
 CC receptor protein, the nucleic acids encoding them, antibodies
 CC raised against them, the fusion proteins between the IgG and IL-13R proteins
 CC and methods of isolating regulators of them. The regulators are useful
 CC for regulating an immune response in a canine. The proteins are useful
 CC to develop regulatory compounds including inhibitors and activators that,
 CC when administered to a canine in an effective manner, are capable of
 CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
 CC regulators are useful for treating canine IgG (heavy and/or light chain)
 CC and/or canine IL-13R mediated responses. The molecules of the invention
 CC are useful to regulate the immune response of an animal (e.g. by gene
 CC therapy). The present sequence is the reverse complement of a cDNA
 CC encoding a protein of the invention.
 XX
 SQ Sequence 1158 BP; 353 A; 224 C; 201 G; 380 T; 0 other;

Query Match 79.6%; Score 1158; DB 22; Length 1158;
 Best Local Similarity 100.0%; Pred. No. 8,1e-261;
 Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 244 ggctctatgcttcaaatgctgagataaaagttaacccctcctcagatgtttgagatagtg 303
 DB 1098 GGCTCTATGCTTTCAAATGCTGAGATAAAAGTTAATCTCCCTCAGGATTTTGAGATAGTG 1039
 QY 304 gacctggatattagggttatctctcttggcaatggcaacctccattatttcggataat 363
 DB 1038 GACCTGGATATTTAGGTTATCTCTTTTGAATGGCAACCTCCATTATTTCCGGATAAT 979
 QY 364 tttaaggatgcacatagaatatagaattaaataccgaaacattgatagtgaactgg 423
 DB 978 TTTAAGGAATGCACATAGAAATGAATTTAAATACCGAAACATTGATAGTGAACACTGG 919
 QY 424 aagaccatcattaccaagaatcattacaaagatgggttgatccttaacaaagtatt 483
 DB 918 AAGACCATCATTTACCAAGAATTTACATTTACAAAGATGGGTTTGATCTTTAACAAAGGTATT 859
 QY 484 gaagcaagataaaacacactcttcgcagcacaatgcacaaatggatcagaagttagaagt 543

DB 858 GAAGCAAAAGATAAACAACACTTTCGCCAGCACAAATGCACAAATGGATCAGAAGTTAGAAGT 799
 QY 544 tcatggcgagaactactcttatggacatcaccacaaggaatcgggaactaaaaattcaa 603
 DB 798 TCATGGCGAGAAACTACTTTATTTGGACATCACCACAGGAATCGGGAACATAAATTCAA 739
 QY 604 gatatggactgtgtatattacaactggcaatatttagtctgtctcttggaaactggcatg 663
 DB 738 GATATGGAGCTGTGTATATTTACAACATGGCAATATTTAGTGTCTTGGAAACCTGGCATG 679
 QY 664 ggtgtccattttgatataccaattaccagttgttttactgtgtatgaggtgtggaccattca 723
 DB 678 GGTGTCCATTTTGATACCAATTTACCAGTTGTCTTACTGTATGAGGGCTTGGACCAATCA 619
 QY 724 gcagagtgtactgattacatcaaggttaatggaaaaataatggatgcagggtttccctat 783
 DB 618 GCAGAGTGTACTGATTTACATCAAGGTTAATGGAAAAAATATGGATGCGAGTTTCCCTAT 559
 QY 784 ttggagtcacagactataaagatttctacatctgtgttaatgggttcacagaatcccgag 843
 DB 558 TTGGAGTTCATCAGACTATAAAGATTTCTACATCTGTGTAAATGGGTTCATCAGAATCCCAG 499
 QY 844 cctatcagaccagctattttatttctcagcttcaaaatatagttaaaactatgccacca 903
 DB 498 CCTATCAGACCCAGCTATTTTATTTTTCAGCTTCAAAATATAGTTAAACCTATGCCACCA 439
 QY 904 gactaccttagtctactgtgaagaattcagagggaattaaacctgaatggaatgcct 963
 DB 438 GACTCTTGTAGTCTTACTGTGAAGAAATTCAGAGGAATTAACCTGAATGGAACATGCCT 379
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 DB 378 AAAGACCCCATTTCCAGCCAAATGTTTCAATTTATGAAATTTGAATTCACAGAGGATGTACT 319
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 QY 1204 ttttttataccatttcttctgtctcaatatttggtttggtaataacttgcctt 1263
 DB 138 TTTTCTTGATACCATTTGCTTTTGTCTCAATATTTTGTGTAATAAATTCCTGCTT 79
 QY 1264 ttgtataagcaaggcttttactgaaaacgatctttcattacacaaaaaagctctttct 1323
 DB 78 TTGTATAAGCAAGGGCTTTACTGAAAACGATCTTTTCATACAAAAAAGAGTCTTTCT 19
 QY 1324 catcaagacacattctgt 1341
 DB 18 CATCAAGACACATTTCTGT 1

RESULT 5

AAS59966

ID AAS59966 standard; cDNA; 1095 BP.

XX AAS59966;

XX AAS59966;

DT 29-JAN-2002 (first entry)

XX Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1095.

DE Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;

KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;

KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;

immune response.
 Canis familiaris.
 WO200177332-A2.
 18-OCT-2001.
 09-APR-2001; 2001WO-US11498.
 07-APR-2000; 2000US-195659P.
 07-APR-2000; 2000US-195874P.
 (HESK-) HESKA CORP.
 McCall CA, Tang L;
 WPI; 2001-657172/75.
 P-PSDB; AAU69136.
 Novel isolated canine protein, preferably canine immunoglobulin G protein or canine interleukin-13 receptor protein useful for regulating immune response of an animal and for developing regulatory compounds -
 Claim 19; Page 179-181; 221pp; English.
 The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13 proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence encodes a protein of the invention.
 Sequence 1095 BP; 370 A; 186 C; 211 G; 328 T; 0 other;

Query Match 75.3%; Score 1095; DB 22; Length 1095;
 Best Local Similarity 100.0%; Pred. No. 4.1e-246;
 Matches 1095; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 tctatgctttcaaatgctgagataaaagttaattctctctcctcaggaatttgagataggac 306
 Db 1 tctatgctttcaaatgctgagataaaagttaattctctcctcaggaatttgagataggac 60
 QY 307 cctggatatttaggttatctctcttgcgaatggcaacctccattatttccggataattt 366
 Db 61 cctggatatttaggttatctctcttgcgaatggcaacctccattatttccggataattt 120
 QY 367 aaggaatgcacaatagaatgaattaaataaccgaacattgtagtgaactggaag 426
 Db 121 aaggaatgcacaatagaatgaattaaataaccgaacattgtagtgaactggaag 180
 QY 427 accatcattaccagaatctacataaagaatgggtttgattcttaacaaaggattgaa 486
 Db 181 accatcattaccagaatctacataaagaatgggtttgattcttaacaaaggattgaa 240
 QY 487 gcaagataaaacacactctgcagcaccaatgcacaaatggatcgagaagttagaattca 546
 Db 241 gcaagataaaacacactctgcagcaccaatgcacaaatggatcgagaagttagaattca 300
 QY 547 tgggcagaactactatttggacatcacacaaggaaatcgggaaactaaattcaaat 606
 Db 301 tgggcagaactactatttggacatcacacaaggaaatcgggaaactaaattcaaat 360
 QY 607 atggactgtgtattacaaactggcaattatttagtctcttggaaacctggcatgggt 666

Db 361 atggactgtgtattacaaactggcaattatttagtctcttggaaacctggcatgggt 420
 QY 667 gtccattttgatcaccaattaccagttgttttactgggtatgagggttgaccattcagca 726
 Db 421 gtccattttgatcaccaattaccagttgttttactgggtatgagggttgaccattcagca 480
 QY 727 gagtgtactgtattacatcaaggttaattgaaaaaaatattggatgcaggtttccctatttg 786
 Db 481 gagtgtactgtattacatcaaggttaattgaaaaaaatattggatgcaggtttccctatttg 540
 QY 787 gagtcatcagactataaagatttctacatctgtttaaattgggttcacagaatcccagcct 846
 Db 541 gagtcatcagactataaagatttctacatctgtttaaattgggttcacagaatcccagcct 600
 QY 847 atcagaccagctattttatttttttcagcttcaaaatattagtttaaacctatgcaccagac 906
 Db 601 atcagaccagctattttatttttttcagcttcaaaatattagtttaaacctatgcaccagac 660
 QY 907 taccttagtcttactgtgaagaattcagaggaattaaacctgaaatggaaatgcactaa 966
 Db 661 taccttagtcttactgtgaagaattcagaggaattaaacctgaaatggaaatgcactaa 720
 QY 967 ggaccattccagcccaaatgtttcatttatgaattgaattcacagaggtgactact 1026
 Db 721 ggaccattccagcccaaatgtttcatttatgaattgaattcacagaggtgactact 780
 QY 1027 tgggtgactaccacagttgagaatgagatcacaaatcacagaacatcaaatgaaagccaa 1086
 Db 781 tgggtgactaccacagttgagaatgagatcacaaatcacagaacatcaaatgaaagccaa 840
 QY 1087 aaattatgcttttttggtaagaagttaaagtgaattatttttctcagatgagaaatctgg 1146
 Db 841 aaattatgcttttttggtaagaagttaaagtgaattatttttctcagatgagaaatctgg 900
 QY 1147 agtgaatgagatgagacaaatgcgtggaagtgcacatggaagaacaccttagtattt 1206
 Db 901 agtgaatgagatgagacaaatgcgtggaagtgcacatggaagaacaccttagtattt 960
 QY 1207 tcttgatcaccattgcttttctcaatatttggtaatttggtaataactgctgcttttg 1266
 Db 961 tcttgatcaccattgcttttctcaatatttggtaatttggtaataactgctgcttttg 1020
 QY 1267 tataagcaaaagggttcttactgaaacgactcttctacaaaaaaagaagctctttctcat 1326
 Db 1021 tataagcaaaagggttcttactgaaacgactcttctacaaaaaaagaagctctttctcat 1080
 QY 1327 caagacacattctgt 1341
 Db 1081 caagacacattctgt 1095

RESULT 6
 AAS59967/c
 ID AAS59967 standard; cDNA; 1095 BP.
 XX
 AC AAS59967;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1095 complement.
 XX
 KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
 IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.
 XX
 OS Canis familiaris.
 XX
 PN WO200177332-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 09-APR-2001; 2001WO-US11498.

XX 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
XX
PA (HESK-) HESKA CORP.
XX
XX McCall CA, Tang L;
XX
XX WPI; 2001-657172/75.
DR
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX Claim 19; Page 183; 221pp; English.
XX
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX
XX Sequence 1095 BP; 328 A; 211 C; 186 G; 370 T; 0 other;
SQ

Query Match 75.3%; Score 1095; DB 22; Length 1095;
Best Local Similarity 100.0%; Pred. No. 4.1e-246;
Matches 1095; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 tctatgcttcaaatgctgagataaaagttaactcctccagattttgagatagtgac 306
Db 1095 TCTATGCTTCAAAATGCTGAGATAAAAGTTAATCTCTCAGGATTTTGAGATAGTGAC 1036

Qy 307 cctggatatagggttatctctcttgcgaatggcaatcccaactccattttccggataatttt 366
Db 1035 CCTGGATATTTAGGTTATCTCTTTGCAATGGCAACCTCCATTATTTCCGGATAATTTT 976

Qy 367 aaggaatcaccaatagaataaataaaataccgaacattgatagtgaaactggag 426
Db 975 AAGGAATGCACAAATAGAATATGAATTAATAATACCGAAACATTTGATAGTGAAACTGGAAG 916

Qy 427 accatcattaccaagaattctacattacaagaatgggtttgatcttcaacaaggatttgaa 486
Db 915 ACCATCATTACCAAGAATCTACATTTACAAGATGGGTTGATCTTTAACAAGATTTGAA 856

Qy 487 gcaagataaaacacacttctgccagcacaaatgcacaaatggatcagaagttagaagtcca 546
Db 855 GCAAAAGATAAACACACTTCTGCCAGCACAAATGCACAAATGGATCAGAAAGTTAGAAGTTCA 796

Qy 547 tgggcagaactactatttgacatcaccaagaagaatcgggaaactaaaattcaagat 606
Db 795 TGGGCAGAAACTACTTATTTGGACATCACCAAGAAATCGGGAAACTAAAATTTCAAGAT 736

Qy 607 atggaactgtatatcaactggcaattatttagtctgctcttgaaacctggcatgggt 666
Db 735 ATGGACTGTGTATATTACACTGGCAATATTAGTCTCTTGGAAACCTTGGCATGGGT 676

Qy 667 gtccattttgataccaattaccagttgttttactggatgagggcttgaccattcacga 726
Db 675 GTCCATTTTGATACCAATTACCAGTTGTTTACTGGTATAGGGCTTGACCATTTCAGCA 616

Qy 727 gagtgtactgtatcatcaaggttaattggaaaaataatgggatgcaggtttccctatttg 786
Db 615 GAGTGTACTGTATTACATCAAGGTTAATGGAAAAATATGGGATGTCAGGTTTCCCTATTGTG 556

Qy 787 gagtcatcagactataaagattttctacatctgttaattgggtcatcagaatcccagcct 846
Db 555 GAGTCATCAGACTATAAAGATTTTCTACATCTGCTGTTAATGGGTCTCAGAAATCCAGCCT 496

Qy 847 atcagaaccagctattttattttttcagcttcaaaatatagtttaaacctatgcccacagac 906
Db 495 ATCAGACCCAGCTATTTTATTTTTCAGCTTCAAAATATAGTTTAAACCTATGCCACAGAC 436

Qy 907 taccttagtcttactgtgaagaattcagaaggaaataaacctgaatgaacatgacctaaa 966
Db 435 TACCTTAGTCTTACTGTGAAGAAATTCAGAGGAAATTAACCTGAAATGGAAATGGCTAAA 376

Qy 967 ggaccattccagccaaaatgttttcatttatgaattgaattccacagagatggttactact 1026
Db 375 GGACCCATTCCAGCCAAAATGTTTCATTTATGAAATTTGAATTCACAGAGGATGGTACTACT 316

Qy 1027 tgggtgactaccacagttgagaatgagatacaaaatacaagaacatcaaatgaaagccaa 1086
Db 315 TGGGTGACTACCACAGTTTGAGAAATGAGATACAAATCACAAGAACATCAAAATGAAAGCCAA 256

Qy 1087 aaattatgcttttggtaagaagtgaattgaattatttctcagatgagaaatctgg 1146
Db 255 AAATTATGCTTTTGGTAAAGAAAGTAAAGTGAATATTTATTTGCTCAGATGATGGAATCTGG 196

Qy 1147 agtggatggatgaacaatgctggaaagtgacatatggaagaaacaccttagtattt 1206
Db 195 AGTGAGTGAGTGATGATGAACAATGCTGGAAAGCTGACATATGGAAGAAACCTTAGTATTT 136

Qy 1207 ttcttgatacaatttgccttttgcataatttggtaatttggtaataacttgcctgcttttg 1266
Db 135 TTCTTTGATACCAATTTGCTTTTCTCAATPATTTGTTTGGTAAATAACTTGCCTGCTTTTG 76

Qy 1267 tataagcaaggcttttactgaaaacgatctttctacatacaaaaaaagaagctcttttctcat 1326
Db 75 TATAAGCAAAAGGCTTTTACTGAAAACGATCTTTTCATACAAAAAAGAGAGCTCTTTTCTCAT 16

Qy 1327 caagcacattctgt 1341
Db 15 CAAGACACATTCTGT 1

RESULT 7
AAS59968
ID AAS59968 standard; cDNA; 954 BP.
XX
AC AAS59968;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine IL-13R extracellular domain cDNA nCaIL-13Ralpha2 954.
XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO2001/7332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI; 2001-657172/75.

DR P-PSDB; AAU69137.
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
PS Claim 19; Page 184-185; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
SQ Sequence 954 BP; 329 A; 162 C; 192 G; 271 T; 0 other;

Query Match 65.2%; Score 947.8; DB 22; Length 954;
Best Local Similarity 99.8%; Pred. No. 9, 2e-212;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 247 tctatgtcttcaaaatgctgagataaaagttaatactctcctcaggattttgagatagtggaac 306
Db 4 tctatgtcttcaaaatgctgagataaaagttaatactctcctcaggattttgagatagtggaac 63
QY 307 cctgcatatttaggttatctctcttgcaatggaatggaacatccattattccggataatttt 366
Db 64 cctgcatatttaggttatctctcttgcaatggaatggaacatccattattccggataatttt 123
QY 367 aagggaatgcacaaatagaatgaattaaataaccgaacattgtagtgaactgggaag 426
Db 124 aagggaatgcacaaatagaatgaattaaataaccgaacattgtagtgaactgggaag 183
QY 427 accatcattaccagaatcattacataaagaatgggttgatctcttaacaaaggattgaa 486
Db 184 accatcattaccagaatcattacataaagaatgggttgatctcttaacaaaggattgaa 243
QY 487 gcaagagataaacacacctctgcagcacacaatgcacaaatggatcagaagttagaagtcca 546
Db 244 gcaagagataaacacacctctgcagcacacaatgcacaaatggatcagaagttagaagtcca 303
QY 547 tgggcagaaactacttatttggacatcacacacaggaataatcgggaaactaaattcaagat 606
Db 304 tgggcagaaactacttatttggacatcacacacaggaataatcgggaaactaaattcaagat 363
QY 607 atggactgtgtattatacaactgggaataatttagtctgctcttgaaacctggcatgggt 666
Db 364 atggactgtgtattatacaactgggaataatttagtctgctcttgaaacctggcatgggt 423
QY 667 gtccattttgataccaataatcacagttgttttactggtatgggcttggaaccttcagca 726
Db 424 gtccattttgataccaataatcacagttgttttactggtatgggcttggaaccttcagca 483
QY 727 gagggtactgattacatacaagtttaattggaaaaataatggggtcagggtttccctattttg 786
Db 484 gagggtactgattacatacaagtttaattggaaaaataatggggtcagggtttccctattttg 543
QY 787 gaggatcagacataaagatttcacatctgtgttaattgggtcattcagaatcccagcct 846
Db 544 gaggatcagacataaagatttcacatctgtgttaattgggtcattcagaatcccagcct 603
QY 847 atcagaccagcattatt 906
Db 604 atcagaccagcattatt 963

RESULT 8
AAS59969/c
ID AAS59969 standard; cDNA; 954 BP.
XX
AC AAS59969;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine IL-13R extracellular domain cDNA nCaIL-13Ralpha2 954 complement.
XX
KW Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG FC;
KW Immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
XX
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI; 2001-657172/75.
XX
PT Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
PS Claim 19; Page 187; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.

```

XX SQ Sequence 954 BP; 271 A; 192 C; 162 G; 329 T; 0 other;
Query Match 65.2%; Score 947.8; DB 22; Length 954;
Best Local Similarity 99.8%; Pred. No. 9.2e-212;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 247 tctatgcttcaaatgctgagataaaagttaatctctcctcaggattttgagatagtgac 306
Db 951 TCTATGCTTTCAAAATGCTGAGATAAAAGTTAATCTCTCCTCAGGATTTTGAGATAGTGAC 892
Qy 307 cctgagattaggttactctcttctgcaatggaaccccatatttcccgataatttt 366
Db 891 CCTGGATATTTAGGTTATCTCTCTTTGCAATGGCAACTCCCATTAATTTCCGGATAATTTT 832
Qy 367 aaggaatcacaaatagaataatgaataaaatcacgaacattgatagtaaaactgggaag 426
Db 831 AAGGAATGCACAATAGATATGAATTAANAATCCGAACATGATAGTGAANAATCGGAAG 772
Qy 427 accatcattaccaagaatctacattacaaagatgggtttgatctttaacaaaggatttgaa 486
Db 771 ACCATCATTTACCAAGATCTACATTTACAAAGATGGTTTGATCTTAACAAAGGTATTGAA 712
Qy 487 gcaaaagataaacacacttctgccagcacaaatgcacaaatgcatcagaagttagaagtcca 546
Db 711 GCAAGATATAACACACTTCTGCCAGCACAAATGCACAAATGGATCATCAGAAAGTTAGAAGTTCA 652
Qy 547 tgggcagaactactatttgacatcaccaagaagaatcggaaactaaattcaagat 606
Db 651 TGGGCAGAAATACCTATTGACATCACCAAGGAATCGGGAACCTAAAATTTCAAGAT 592
Qy 607 atggactgttatattacaactggcaatatttagtctctcttggaaacctggcagtggt 666
Db 591 ATGGACTGTATATTACAACCTGGCAATATTTAGTCTGCTCTTGGAACCTGGCATGGGT 532
Qy 667 gtccatttgcatacaaatcacagttgttactggtgatgagggttgaccattcagca 726
Db 531 GTCCATTTTGTACCAATTTACCAAGTTGTTTACTGGTATGAGGGCTTGGACCATTCAGCA 472
Qy 727 gagtgtactgtattacatcaagtttaagtgaataatggaatcaggtttccctatttg 786
Db 471 GAGTGTACTGATTACATCAAGTTAATGGAATAATATGGAATGATGAGGTTTCCCTATTTG 412
Qy 787 gagtcatcagactaaaagatttctacatctgtgttaattgggtcgtatcagaatcccgact 846
Db 411 GAGTCATCAGACTATAAGATTTCTACATCTGTGTAAATGGTCTATCAGAAATCCAGCCT 352
Qy 847 atcagaccagctatttctatttgcagtttcaaaaatagtttaaacctatgcccacagac 906
Db 351 ATCAGACCCAGCTATTTTATTTTTCAGCTTCAAAAATATAGTTAAACCTATGACCACAGAC 292
Qy 907 taccttagttactgtgaagaattcagaggaaaataaccctgaaatggaacatgctctaaa 966
Db 291 TACCTTAGTCTTACTGTGAAGAATTCAGAGGAAATTAACCTGAAATGGAACATGCTCTAAA 232
Qy 967 ggaccctatccagccaaatgttccatttatgaaattgaattcacagaggttggttactact 1026
Db 231 GGACCCATTCAGCCCAATGTTTCATTATGNAATGGAATTCACAGAGATGGTACTACT 172
Qy 1027 tgggtgactaccacagttgagaatgagatacaaaatcacaaagaacatcaaatgaaagccaa 1086
Db 171 TGGGTGACTACACAGTTTGAGAATGAGATACAAATCACAAAGAACATCAAAATGAAAGCCAA 112
Qy 1087 aaattatgcttttggtaagaagtaaaagtgaataatttatttgcctcagatgagtaactcgg 1146
Db 111 AAATTTATGCTTTTGGTAAGAAGTAAAGTGAATATATTTTATGCTCAGATGATGGAATCTGG 52
Qy 1147 agtgaagtgaatgaacaatgctggaaagtgacatgatgaaagaaacc 1197
Db 51 AGTGAGTGGAGTGTATCAACAATGCTTGGAAAGGTGATATCTCTGGAAGAAACC 1

Novel isolated canine protein, preferably canine immunoglobulin G
protein or canine interleukin-13 receptor protein useful for regulating
immune response of an animal and for developing regulatory compounds -
Claim 37; Page 187-190; 221pp; English.
The invention concerns an isolated canine protein, preferably canine
immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
receptor protein, the nucleic acids encoding them, antibodies
raised against them, fusion proteins between the IgG and IL-13 proteins
and methods of isolating regulators of them. The regulators are useful
for regulating an immune response in a canine. The proteins useful to
develop regulatory compounds including inhibitors and activators that,
when administered to a canine in an effective manner, are capable of
protecting canine from disease mediated by IL-13Ralpha or IL-13. The
regulators are useful for treating canine IgG (heavy and/or light chain)
and/or canine IL-13R mediated responses. The molecules of the invention
are useful to regulate the immune response of an animal (e.g. by gene
therapy). The present sequence encodes a protein of the invention.
Sequence 1686 BP; 513 A; 384 C; 382 G; 407 T; 0 other;
Query Match 65.2%; Score 947.8; DB 22; Length 1686;
Best Local Similarity 99.8%; Pred. No. 1.1e-211;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 247 tctatgcttcaaatgctgagataaaagttaatctctcctcaggattttgagatagtgac 306
Db 4 tctatgcttcaaatgctgagataaaagttaatctctcctcaggattttgagatagtgac 63
Qy 307 cctgagatttaggttattctctcttgcgaatggcaacctccattttcccgataatttt 366
Db 64 cctgagatttaggttattctctcttgcgaatggcaacctccattttcccgataatttt 123
Qy 367 aaggaatcacaaatagaataatgaataaaatcacgaacattgatagtaaaactgggaag 426
Db 124 aaggaatgcacaatagaaatgaataaaatcacgaacattgatagtaaaactgggaag 183
Qy 427 accatcattaccaagaatctacattacaagaatgggtttgatctttaacaaaggatttgaa 486
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Db 184 accatcattaccaagaattacattacaaagatgggttgattcttaacaaaggtattgaa 243
QY 487 gcaagataaaacacactcttcgcagcacaaatgcacaaatgctgagaagttagaagtcca 546
Db 244 gcaagataaaacacactcttcgcagcacaaatgcacaaatgctgagaagttagaagtcca 303
QY 547 tgggcagaaactcacttatttggacatcacacacaggaatcgggaaactaaatccaagt 606
Db 304 tgggcagaaactcacttatttggacatcacacacaggaatcgggaaactaaatccaagt 363
QY 607 atggactgtgtattatacaactggcgaatatattagctgctcttggaaacctggcatgggt 666
Db 364 atggactgtgtattatacaactggcgaatatattagctgctcttggaaacctggcatgggt 423
QY 667 gtccattttgatcaccaattaccagttgttttactggtatgagggcttggaccattcagca 726
Db 424 gtccattttgatcaccaattaccagttgttttactggtatgagggcttggaccattcagca 483
QY 727 gsgtgcactgattacatcaagggttaatgggaaaaaatatgggatgcaggtttccctatttg 786
Db 484 gsgtgcactgattacatcaagggttaatgggaaaaaatatgggatgcaggtttccctatttg 543
QY 787 gsgtgcactgacataaaagatttctacatctgtgttaattgggtcatcagaatccccagcct 846
Db 544 gsgtgcactgacataaaagatttctacatctgtgttaattgggtcatcagaatccccagcct 603
QY 847 atcaaccacagctatttatttttcagcttcaaaatatagtttaaacctatgccacagac 906
Db 604 atcaaccacagctatttatttttcagcttcaaaatatagtttaaacctatgccacagac 663
QY 907 taccttagtcttactgtggaattcagaggaattaaactgaaatggaacatgcctaaa 966
Db 664 taccttagtcttactgtggaattcagaggaattaaactgaaatggaacatgcctaaa 723
QY 967 gaaccattcccgccaaatgttccatttataatgaattgaattcacagaggtggtactact 1026
Db 724 gaaccattcccgccaaatgttccatttataatgaattgaattcacagaggtggtactact 783
QY 1027 tgggtgactcacacagtttgagaatgagatcacaaatcacagaacatcaaatgaagccaa 1086
Db 784 tgggtgactcacacagtttgagaatgagatcacaaatcacagaacatcaaatgaagccaa 843
QY 1087 aaattatgcttttttggtaagaagtaaaagtgaaattatttattgctcagatgatggaactgg 1146
Db 844 aaattatgcttttttggtaagaagtaaaagtgaaattatttattgctcagatgatggaactgg 903
QY 1147 agtgggtggagtgtgaacaaatgctggaaaggtgacatatgaaaggaacc 1197
Db 904 agtgggtggagtgtgaacaaatgctggaaaggtgacatatgaaaggaacc 954
```

```
RESULT 10
AAS59971/c
ID AAS59971 standard; cDNA; 1686 BP.
XX
AC AAS59971;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine IL-13Ralpha2/IgG-Fc fusion protein cDNA reverse complement.
XX
KW Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW Immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
```

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PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI; 2001-657172/75.
XX
XX
Novel isolated canine protein, preferably canine immunoglobulin G
protein or canine interleukin-13 receptor protein useful for regulating
immune response of an animal and for developing regulatory compounds -
Example 4; Page 193-194; 221pp; English.
PS
XX
CC The invention concerns an isolated canine protein, preferably canine
immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
receptor protein, the nucleic acids encoding them, antibodies
raised against them, fusion proteins between the IgG and IL-13R proteins
and methods of isolating regulators of them. The regulators are useful
for regulating an immune response in a canine. The regulators are useful
to develop regulatory compounds including inhibitors and activators that,
when administered to a canine in an effective manner, are capable of
protecting canine from disease mediated by IL-13Ralpha or IL-13. The
regulators are useful for treating canine IgG (heavy and/or light chain)
and/or canine IL-13R mediated responses. The molecules of the invention
are useful to regulate the immune response of an animal (e.g. by gene
therapy). The present sequence is the reverse complement of a cDNA
encoding a protein of the invention.
XX
SQ Sequence 1686 BP; 407 A; 382 C; 384 G; 513 T; 0 other;
Query Match 65.2%; Score 947.8; DB 22; Length 1686;
Best Local Similarity 99.8%; Pred. No. 1.1e-211;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 247 tctatgcttccaaagctgagataaaaagtttaactctctcagagattttgagatagtggaac 306
Db 1683 TCTATGCTTTCAAAATGCTGAGATAAAAAGTTAATCTCTCCAGGATTTTGAGATAGTGGAC 1624
QY 307 cctggatatttaggttatctctcttgaatggcaacctccattatttccggataatttt 366
Db 1623 CTGGATATTAGGTATCTCTTTGCATGCGAACCTCCATTTATTCGGGATAATTTT 1564
QY 367 aaggaatgcacaatagaatatgaattaaaaatcccaaacattgatgtgaaactggaag 426
Db 1563 AAGGAATGCACAATAGATATGAATTAATAATACCGAAACATTTGATAGTGAACCTGGAAG 1504
QY 427 accatcattaccaagaattacattacaaagatgggttttgattcttaacaaaggtattgaa 486
Db 1503 ACCATCATTACCAAGAATCTACATTACAAAGATGGGTGTTGATCTTTAACAAAGGTATTGAA 1444
QY 487 gcaagataaaacacacacttctgcagcacaaatgcacaaatggatcagaagttagaagtcca 546
Db 1443 GCAAGATAAAACACACTTCTGCCAGCACAAATGCACAAATGGATCAGAGTTAGAGTTCA 1384
QY 547 tgggcagaaactcacttatttggacatcacacacaggaatcgggaaactaaatccaagt 606
Db 1383 TGGGCGAAACACTTACTATTGGACATCACCCACAAAGGAAATCGGGAAACTAAAATTCAGAT 1324
QY 607 atggactgtgtattatacaactggcgaatatattagctgctcttggaaacctggcatgggt 666
Db 1323 ATGGACTGTGTATATTACAACTGGCAATATTTAGTCTGTCTCTTGGAAACCTGGCATGGGT 1264
QY 667 gtccattttgatcaccaattaccagttgttttactggtatgagggcttggaccattcagca 726
Db 1263 GTCCATTTTGATACCAATTTACCAGTTGTTTACTGGTATGAGGGCTTGGACCATTCAGA 1204
QY 727 gagtgtactgtattacatcaaggttaattgaaaaaatatggaatgaggtttccctatttg 786
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QY 1087 aaattatgcttttggtaagaagtaaaagtgaatattatttattgctcagatgatgaaactgg 1146
 |||||||
 Db 844 aaattatgcttttggtaagaagtaaaagtgaatattatttattgctcagatgatgaaactgg 903
 |||||||
 QY 1147 agtgaagtgagtgatgaacaactgctggaagtgacatgatggaagaaacc 1197
 |||||||
 Db 904 agtgaagtgagtgatgaacaactgctggaagtgacatgatggaagaaacc 954
 |||||||

RESULT 12
 AAS59977/c
 ID AAS59977 standard; cDNA; 1686 BP.
 XX
 AC AAS59977;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Canine IL-13Ralpha2/IgG-Fc fusion protein cDNA reverse complement #4.
 XX
 KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
 IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.
 XX
 OS Canis familiaris.
 XX
 PN WO200177332-A2.
 XX
 PD 18-OCT-2001.
 XX
 XX 09-APR-2001; 2001WO-US11498.
 XX
 PR 07-APR-2000; 2000US-195659P.
 PR 07-APR-2000; 2000US-195874P.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI McCall CA, Tang L;
 XX
 DR WPI; 2001-657172/75.
 XX
 XX Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -
 XX
 PS Claim 37; Page 212-213; 221pp; English.
 XX
 CC The invention concerns an isolated canine protein, preferably canine
 CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
 CC receptor protein, the nucleic acids encoding them, antibodies
 CC raised against them, fusion proteins between the IgG and IL-13 proteins
 CC and methods of isolating regulators of them. The regulators are useful
 CC for regulating an immune response in a canine. The proteins useful to
 CC develop regulatory compounds including inhibitors and activators that,
 CC when administered to a canine in an effective manner, are capable of
 CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
 CC regulators are useful for treating canine IgG (heavy and/or light chain)
 CC and/or canine IL-13R mediated responses. The molecules of the invention
 CC are useful to regulate the immune response of an animal (e.g. by gene
 CC therapy). The present sequence is the reverse complement of a cDNA
 CC encoding a protein of the invention.
 XX
 SQ Sequence 1686 BP; 407 A; 379 C; 388 G; 512 T; 0 other;

Query Match 65.2%; Score 947.8; DB 22; Length 1686;
 Best Local Similarity 99.8%; Pred. No. 1.1e-211;
 Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 247 tctatgcttcaaaagtctgagataaaaagttaactctctccacaggattttgagatagtgac 306
 |||||||
 Db 1683 TCTATGCTTTCAATGCTGAGATAAAAGTTAATCTCTCCCTCAGGATTTTGAGATAGTGGAC 1624
 |||||||

QY 307 cctggatatttaggttatctctcttgcgaatggcaacctccattatttccggataatttt 366
 |||||||
 Db 1623 CCTGGATATTTAGGTATATCTCTCTTTGCAATGGCAACCTCCATATTTTCGGGATAATTTT 1564
 |||||||
 QY 367 agggaaatgcacaatagaatatgaattaaaataccgaaacatttgatagtgaaaactggaag 426
 |||||||
 Db 1563 AAGGAATGCACAATAGAATATGAATTTAAATACCGAAACATTCATAGTGAANAATCGAAG 1504
 |||||||
 QY 427 accatcattaccaagaatctacatttcaaaagatgggtttgatcttcaaaagattatgaa 486
 |||||||
 Db 1503 ACCATCATTTACCAAGAATCTACATTTACAAAGATGGGTTTGATCTTAAACAAGGTATTGAA 1444
 |||||||
 QY 487 gcaaaagataaaacacactctgccagcacaaatgcacaaatggatcagaagttaagaattca 546
 |||||||
 Db 1443 GCAAAAGATAAACACACTTCTGCCGAGCACAAATGCACAAATGGATCAGAAGTTGAAAGTTCA 1384
 |||||||
 QY 547 tgggcgaactacttatttggacatcaccacaaggaaatcgggaaactaaaaattcaaat 606
 |||||||
 Db 1383 TGGGCAGAAACTACTTATTGGACATCACCACAGGAAATCGGGAAACTAAAATTCAGAT 1324
 |||||||
 QY 607 atggactgtgtatattacaaactggcaatatttagtctgtctcttggaaacctggcatgggt 666
 |||||||
 Db 1323 ATGGACTGTGTATATTACAACCTGGCAATATTTAGTCTGCTCTTTGGAAACCTGGCATGGGT 1264
 |||||||
 QY 667 gtccatttggataccaattaccagttgttttactgtgtatgagggtcttgaccattcagca 726
 |||||||
 Db 1263 GTCCATTTTGATACCAATTTACCAGTTGTTTACTGTGTATGAGGGCTTGGACCATTCAGA 1204
 |||||||
 QY 727 gagtgtactgattacatcaagggttaatggaaaaaaatgggatggcaggtttccctatttg 786
 |||||||
 Db 1203 GAGTGTACTGATTACATCAAGGTTAATGGAAAAAATATGGGATGCAGGTTTCCCTATTTC 1144
 |||||||
 QY 787 gagtcatcagactataaaagatttctacatctgtgttaatgggttcacagaatccccagcct 846
 |||||||
 Db 1143 GAGTCATCAGACTATAAAGATTTCTACATCTGTGTAAATGGGTCTATCAGAAATCCCAGCCT 1084
 |||||||
 QY 847 atcagacccagctatttttacttttcagcttcaaaatattagttaaaacctatgcaccagac 906
 |||||||
 Db 1083 ATCAGACCCAGCTATTTTATTTTTCAGCTTCAAAATATAGTTAAACCTATGCCACCAGAC 1024
 |||||||
 QY 907 taccctagttactgtgaagaattcagaggaaattaaacctgaaatggacaatgcctaaa 966
 |||||||
 Db 1023 TACCTTAGTCTTACTGTGAAGAAATTCAGAGGAAATTAACCTGAAATGGAACATGCCTAAA 964
 |||||||
 QY 967 gaccattccagccaaaatgtttcatttgaattgaattgaattcacagagatggctactact 1026
 |||||||
 Db 963 GGACCCCATTTCCAGCCAAATGTTTCATTTATGAAATTTGAATTCACAGAGGATGGTACTACT 904
 |||||||
 QY 1027 tgggtgactaccacagttgagaatgagatcacaaatcacagaacatcaaatgaaagccaa 1086
 |||||||
 Db 903 TGGGTGACTACCCACAGTTGAGAAATGAGATCAAAATCCAAAGAACATCAAAATGAAGCCAA 844
 |||||||
 QY 1087 aaattatgcttttggtaagaagtaaaagtgaatatttatttgcagatgatgaaactgg 1146
 |||||||
 Db 843 AAATATTGCTTTTGGTAAAGAGTAAAGTGAATATTTATTTGCTCAGATCATGGAATCTGG 784
 |||||||
 QY 1147 agtgaagtgagtgatgaacaactgctggaagtgacatgatggaagaaacc 1197
 |||||||
 Db 783 AGTGAAGTGGAGTGATGAACAATCTGGAAGGTGATATCTCTGGAAGGAAACC 733
 |||||||

RESULT 13
 AAS59974
 ID AAS59974 standard; cDNA; 1692 BP.
 XX
 AC AAS59974;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Canine IL-13R/IgG-Fc fusion protein cDNA nCaIL-13Ralpha2-Fc-B9 1689.
 XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
 KW

KW IL-13Ralphal; IR-13Ralphal; Immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.

OS Canis familiaris.

XX WO200177332-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001WO-US11498.

XX 07-APR-2000; 2000US-195659P.

XX 07-APR-2000; 2000US-195874P.

XX (HESK-) HESKA CORP.

XX McCall CA, Tang L;

XX WPI; 2001-657172/75.

XX P-PSDB; AAU69140.

XX Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -
 XX
 XX Claim 37; Page 200-203; 221pp; English.

XX The invention concerns an isolated canine protein, preferably canine
 CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
 CC receptor protein, the nucleic acids encoding them, antibodies
 CC raised against them, fusion proteins between the IgG and IL-13R proteins
 CC and methods of isolating regulators of them. The regulators are useful
 CC for regulating an immune response in a canine. The proteins useful to
 CC develop regulatory compounds including inhibitors and activators that,
 CC when administered to a canine in an effective manner, are capable of
 CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
 CC regulators are useful for treating canine IgG (heavy and/or light chain)
 CC and/or canine IL-13R mediated responses. The molecules of the invention
 CC are useful to regulate the immune response of an animal (e.g. by gene
 CC therapy). The present sequence encodes a protein of the invention.
 XX
 XX Sequence 1692 BP; 518 A; 376 C; 385 G; 413 T; 0 other;

Query Match 65.2%; Score 947.8; DB 22; Length 1692;
 Best Local Similarity 99.8%; Pred. No. 1.1e-211;
 Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 247 tctatgcttcaaatgctgagataaaagttaatctctctcaggattttgagatagtgagac 306

Db 4 tctatgcttcaaatgctgagataaaagttaatctctcaggattttgagatagtgagac 63

Qy 307 cctggatattaggttatctctcttgcgaatggcaacacctcattattccggataatttt 366

Db 64 cctggatattaggttatctctcttgcgaatggcaacacctcattattccggataatttt 123

Qy 367 aaggatgcacaatagataatgaatataaacacgaaacattgatagtgaaactgggaag 426

Db 124 aaggatgcacaatagataatgaatataaacacgaaacattgatagtgaaactgggaag 183

Qy 427 accatcattacaagaatctcattacaaagatgggtttgatcttcaacaaggtattgaa 486

Db 184 accatcattacaagaatctcattacaaagatgggtttgatcttcaacaaggtattgaa 243

Qy 487 gcaagaataaacacacttctgccagcacaatgcacaaatggatcagaagttagaagtcca 546

Db 244 gcaagaataaacacacttctgccagcacaatgcacaaatggatcagaagttagaagtcca 303

Qy 547 tgggcagaactactatttgacatcacacaaagaaatcgggaaactaaaattcaagat 606

Db 304 tgggcagaactactatttgacatcacacaaagaaatcgggaaactaaaattcaagat 363

Qy 607 atggactgtgtatattacaactggcaatatttagtctgtcttggaaacctggcatgggt 666
 Db 364 atggactgtgtatattacaactggcaatatttagtctgtcttggaaacctggcatgggt 423

Qy 667 gtccattttgatacaaataccagttgttttactagttagggcttgacattcagca 726

Db 424 gtccattttgatacaaataccagttgttttactagttagggcttgacattcagca 483

Qy 727 gagtgtactgattacatcaaggttaattgaaaaataatggatgcaggtttccctatttg 786

Db 484 gagtgtactgattacatcaaggttaattgaaaaataatggatgcaggtttccctatttg 543

Qy 787 gagtcatcagactataaagattttctacatctgtgttaattggttcacagaatccagcct 846

Db 544 gagtcatcagactataaagattttctacatctgtgttaattggttcacagaatccagcct 603

Qy 847 atcagaccagctattttatttttcagcttcaaaatataatagtttaaaccctatgccaccagac 906

Db 604 atcagaccagctattttatttttcagcttcaaaatataatagtttaaaccctatgccaccagac 663

Qy 907 taccttagtcttactgtgaagaattcagagaaaataaacctgaaatggaacatgcctaaa 966

Db 664 taccttagtcttactgtgaagaattcagagaaaataaacctgaaatggaacatgcctaaa 723

Qy 967 ggaccattccagccaaatgttttcatttatgaaattgaattcacagagagatgggtactact 1026

Db 724 ggaccattccagccaaatgttttcatttatgaaattgaattcacagagagatgggtactact 783

Qy 1027 tgggtgactaccacagttgagaatgagatacaaaatcacagaacatcaaatgaaagccaa 1086

Db 784 tgggtgactaccacagttgagaatgagatacaaaatcacagaacatcaaatgaaagccaa 843

Qy 1087 aaattatgctttttgttgaagaatgaagtgaattatttctcagatgagtggaatctgg 1146

Db 844 aaattatgctttttgttgaagaatgaagtgaattatttctcagatgagtggaatctgg 903

Qy 1147 agtgagtgagtgatgcacaatgctggaaggtgcacatggaaggaagaaacc 1197

Db 904 agtgagtgagtgatgcacaatgctggaaggtgcacatggaaggaagaaacc 954

RESULT 14

AAS59975/C

ID AAS59975 standard; cDNA; 1692 BP.

XX AAS59975;

XX 29-JAN-2002 (first entry)

XX Canine IL-13Ralphal2/IgG-Fc fusion protein cDNA reverse complement #3.

XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;

XX IL-13Ralphal; IR-13Ralphal2; Immunoglobulin heavy chain; IgG Fc;

XX immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;

XX immune response.

XX Canis familiaris.

XX WO200177332-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001WO-US11498.

XX 07-APR-2000; 2000US-195659P.

XX 07-APR-2000; 2000US-195874P.

XX (HESK-) HESKA CORP.

XX McCall CA, Tang L;

XX WPI; 2001-657172/75.

Novel isolated canine protein, preferably canine immunoglobulin G protein or canine interleukin-13 receptor protein useful for regulating immune response of an animal and for developing regulatory compounds - Example 4; Page 206; 221pp; English.

The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13R proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence is the reverse complement of a cDNA encoding a protein of the invention.

Sequence 1692 BP; 413 A; 385 C; 376 G; 518 T; 0 other;

Query Match 65.2%; Score 947.8; DB 22; Length 1692;
Best Local Similarity 99.8%; Pred. No. 1.le-211;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 247 tctatgctttcaaatgctgagataaagtaaatcctcctcagagattttgacatagtgcac 306
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1589 TCTATGCTTTCAAAATGCTGAGATAAAGTAAATCCTCTCAGAGATTTTGAGATAGTGGAC 1630
QY 307 cctggatatttaggttatctctctttgcaa tggcaacctccattatttcccgataatttt 366
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1629 CTTGGATATTTAGGTATCTCTCTTGGCAATGGCAACCTCCATTATTTCCGGATAATTTT 1570
QY 367 aaggaatgcacaa tagaatatgaattaaaa taccgaaacatctgatagtgaaaaatggaag 426
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1569 AAGGAATGCACAAATAGAAATATGAATTAATAATACGGAACAACTGTAGTGAATACTGGAAG 1510
QY 427 acctattaccagaactctacatcagaagatgggttttgatcttcaaaaggtatgaa 486
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1509 ACCATCATTTACCAAGATCTACATTTACAAAGTGGGTTTGATCTTTACAAAGGTATTGAA 1450
QY 487 gcaagataaaacacactctctgcagacaaatgcgcaaaatggatcagaagtttagaagttca 546
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1449 GCAAAAGATAAACACACATCTGCCAGCACAAATGCACAAATGGATCAGAAGTTAGAAGTTCA 1390
QY 547 tgggcagaaactaactatttggagacatcccaacaaaggaatacgggaaactaaataatcaagat 606
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1389 TGGGCAGAAACTACTTATTTGGACATCACACAGGAAATCGGGAACTTAAATTTCAAGAT 1330
QY 607 atggactgtgatattacaactggcgaatattagctctcttggaaacctggcatgggt 666
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1329 ATGGACTGTGTATTTACAACTGGCAATATTTAGTCTGCTCTTGGAAACCTTGGCATGGGT 1270
QY 667 gtccattttgataccaattaccagttgttttacttggttatgggcttggaccattccagca 726
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1369 GTCCATTTTGATACCAATTTACCAGTTGTTTACTTGGTATGAGGGCTTGGACCAATTCAGCA 1210
QY 727 gagtgactgattacatacaagggttaattggaataaataatgggatcaggtttccctatttg 786
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1209 GAGTGTACTCATTTACATCAAGGTTTAATGGAAAAAATATGGGATCGAGTTTCCCTATTG 1150
QY 787 gagtcatcaactataaagatttctacatctgttgaatgggtcatcagaatccagcct 846
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1149 GAGTCACTCAGACTATAAAGATTTCTACATCTGTGTATTTGGGTCTATCAGAAATCCAGGCT 1090
QY 847 atcagaccagctattttattttcagcttcaaaata tagttaaaccttatgccaccagac 906
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1089 ATCAGACCCAGCTATTATTTATTTTTCAGCTTCAAAATATAGTTAAACCTTATGCCACCAGAC 1030
QY 907 taccttagtcttactgtgaagaaatccagaggaataatcaacctgaaatgggaacatgcataa 966

SQ Sequence 1698 BP; 522 A; 383 C; 388 G; 405 T; 0 other;

Query Match 65.2%; Score 947.8; DB 22; Length 1698;
Best Local Similarity 99.8%; Pred. No. 1.le-211;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 247 tctatgcttccaatgcgagataaaagttaactctcctcaggatttgagatagtggaac 306
DB 4 tctatgcttccaatgcgagataaaagttaactctcctcaggatttgagatagtggaac 63
QY 307 cctggatatttaggttattctctcttcttgcaatggcaacctccattatttccggataatttt 366
DB 64 cctggatatttaggttattctctcttcttgcaatggcaacctccattatttccggataatttt 123
QY 367 aaggaaatgcacaatagaatataaataaccgaacacattgatagtgaaacactgggaag 426
DB 124 aaggaaatgcacaatagaatataaataaccgaacacattgatagtgaaacactgggaag 183
QY 427 accatattaccaagaatctacattacaagaatgggtttgtactttaacaaaaggtattgaa 486
DB 184 accatattaccaagaatctacattacaagaatgggtttgtactttaacaaaaggtattgaa 243
QY 487 gcaagataaacacactctgcagacacaaatgcacaaaatggatcagaaagttagaagttca 546
DB 244 gcaagataaacacactctgcagacacaaatgcacaaaatggatcagaaagttagaagttca 303
QY 547 tgggcagaaactacttattggacatccaccagaagaaatcgggaaactaaaattccaagat 606
DB 304 tgggcagaaactacttattggacatccaccagaagaaatcgggaaactaaaattccaagat 363
QY 607 atggactgtgtattacaactggcaattatttagtctgtctcttgaaacctggcatgggt 666
DB 364 atggactgtgtattacaactggcaattatttagtctgtctcttgaaacctggcatgggt 423
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Job time: 17356 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 15:11:35 ; Search time 5720.3 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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VERSION	AF314533.1	AF314533.1	1454 bp	mrna	linear	MAM 16-OCT-2001	
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AUTHORS	Tang, L.	Tang, L.	1454 bp	mrna	linear	MAM 16-OCT-2001	
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JOURNAL	Vet. Immunol. Immunopathol. 79 (3-4), 181-195 (2001)	Vet. Immunol. Immunopathol. 79 (3-4), 181-195 (2001)	1454 bp	mrna	linear	MAM 16-OCT-2001	
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TITLE	Direct Submission	Direct Submission	1454 bp	mrna	linear	MAM 16-OCT-2001	

JOURNAL Submitted (18-OCT-2000) Allergy and Immunology, Heska Corporation,
1613 Prospect Parkway, Fort Collins, CO 80525, USA
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ACCESSION AX280325
VERSION AX280325.1 GI:16607703
KEYWORDS
SOURCE dog.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)

AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 60 18-OCT-2001;
Heska Corporation (US)
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REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 62 18-OCT-2001;

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QY	1021	actacttgggtactaccacagttgagaatgagatacaaatcacagaacatcaaatgaa	1080		
DB	434	ACTACTTGGGTGACTACCCAGTTGAGATGAGATACAATCACAAGAACATCAAAATGAA	375		
QY	1081	agccaaaaattatgcttttggtaagaagtaaaagtgaattatttattgtcagatgatgga	1140		
DB	374	AGCCAAAATATTGCTTTTGGTAAGAAGTAAAGTGAATATTATTATGCTCAGATGATGGA	315		
QY	1141	atctggagtgtgagtgatgaacaaatcgtggaagggtgacatacggagaagaaacctta	1200		
DB	314	ATCTGGAGTGAGTGGAGTGATGAACAATGCTGAAAAGTGACATATGGAAGGAACCTTA	255		
QY	1201	gtattttcttgataccatttctgttctcaatttctcaatttctgttaacttgcctg	1260		
DB	254	GTAATTTCTTGATACCATTTGCTTTTGTCTCAATATTGTTTGGTAATACTGCCCCTG	195		
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DB	194	CTTTTGTATAAGCAAGGCTTTACTGAAAACGATCTTTCATACAAAAGAAAGTCTTT	135		
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QY	1381	atgagctcttataaacctgaagcttttcccaaatcttcaataattgaataacttatttaaaaga	1440		
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LOCUS	AX280328	Sequence 63 from Patent WO0177332.	1158 bp	DNA	linear
DEFINITION					
ACCESSION	AX280328				
VERSION	AX280328.1	GI:16607706			
KEYWORDS					
SOURCE		dog.			
ORGANISM		Canis familiaris			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
		Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
REFERENCE		1 (sites)			
AUTHORS		Mccall,C.A. and Tang,L.			
TITLE		Compositions and methods related to canine igg and canine il-13			
JOURNAL		receptors			
		Patent: WO 0177332-A 63 18-OCT-2001;			
		Heska Corporation (US)			
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QY	184	atggcttcttctcattcattgagtcggattccctctacaccttctgtttgtccagcagattt	243		
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Qy 244 ggctctatgctttcaaatgctgagataaaaagttaatcctcctcagattttgagatagtg 303
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Qy 364 ttaagggaatcaccaatagatatgaattaaatcaccaaacattgtagtgaactgg 423
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Db 1141 CATCAAGACACATTCTGT 1158
RESULT 5
LOCUS AX280329/c
DEFINITION Sequence 64 from Patent WO0177332.
ACCESSION AX280329
VERSION AX280329.1 GI:16607707
KEYWORDS dog.
SOURCE
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine lgg and canine ll-13 receptors
JOURNAL Patent: WO 0177332-A 64 18-OCT-2001;
Heska Corporation (US)
FEATURES
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/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 353 a 224 c 201 g 380 t
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Query Match 79.6%; Score 1158; DB 6; Length 1158;
Best Local Similarity 100.0%; Pred. No. 1.2e-224;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 184 atggtttcattcatttgatgctcgattcctctataccctgctgtttgacacacattt 243
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Qy 244 ggctctatgctttcaaatgctgagataaaaagttaatcctcctcagattttgagatagtg 303
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Qy 424 aagaccatcattaccaagaattcacattacaagaatgggtttgatctttaacaaaggattt 483
Db 918 AAGACCATCATTTACCACAAATCTACATTTACAAGATGGTGTGATCTTAAACAAAGGTATT 859
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Qy 724 gcaagtgactgattacatcaaggttaatggaaaaaataatgggatgcaggtttccctcat 783
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BASE COUNT	329 a	162 c	192 g	271 t	
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Query Match	65.2%	Score 947.8;	DB 6;	Length 954;	
Best Local Similarity	99.8%;	Pred. No. 4.3e-182;			
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QY	307	cctggtattttagggttatctctctcttgcgaatggcaacctccattatttccggataatttt	366		
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QY	487	gcaagaataaacacactctctgcagcacaatgacacaaatggatcagaagtttagaagtcca	546		
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QY	547	tggcgagaactcaattattgggacatcaccaacaaggaaatcgggaaactaaataccaagt	606		
Db	304	TGGCGAGAAACACTACTTTTGGACATCACCAAGGAAATCGGGAACTTAAATATCAAGAT	363		
QY	607	atggactgttatatacaactcggcaatatattgctctctcttgaaacctggcatgggt	666		
Db	364	ATGGACTGTGTATATTACAACTGGCAATATTTAGTCTGCTCTTGAAACCTGGCATGGGT	423		
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Db	424	GTCCATTTTGATACCAATTAACAGTTGTGTTTACTGGTATGAGGGCTTGGACCATTCAGCA	483		
QY	727	gagtgactgataacatcaaggttaatggaaaaataatgggagtgaggtttccctatttg	786		
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QY	787	gagtcacagactataaagattctacatctgtgttaatgggtcgcacagaatccccagct	846		
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QY	907	tacotttagcttactgtgaagaatcagaaggaaataaacctgaaatggaacatgcctaaa	966		
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LOCUS	AX280335	Sequence 70 from Patent WO0177332.	954 bp	DNA	linear
DEFINITION	AX280335	Sequence 70 from Patent WO0177332.			
ACCESSION	AX280335				
VERSION	AX280335.1	GI:16607713			
KEYWORDS					
SOURCE	dog,				
ORGANISM	Canis familiaris				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
TITLE	1 (sites)				
JOURNAL	McCalli,C.A. and Tang,L.				
FEATURES	Compositions and methods related to canine igg and canine il-13				
source	receptors				
BASE COUNT	Patent: WO 0177332-A 70 18-OCT-2001;				
ORIGIN	Heska Corporation (US)				
	Location/Qualifiers				
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Query Match	65.2%	Score 947.8;	DB 6;	Length 954;	
Best Local Similarity	99.8%;	Pred. No. 4.3e-182;			
Matches 949;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	247	tctatgctttcaaatgctgagataaaagttaatctctcctcagattttgagataaggac	306		
Db	951	TCTATGCTTTCAAAATGCTGAGATAAAGTTAATCTCTCCTCAGGATTTTGAGATAGTGGAC	892		
QY	307	cctggtattttagggttatctctctcttgcgaatggcaacctccattatttccggataatttt	366		
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QY	487	gcaagaataaacacactctctgcagcacaatgacacaaatggatcagaagtttagaagtcca	546		
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (sites)
Mccall,C.A. and Tang,L.
Compositions and methods related to canine igg and canine il-13
receptors
Patent: WO 0177332-A 73 18-OCT-2001;
Heska Corporation (US)
Location/Qualifiers
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/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 407 a 382 c 384 g 513 t
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Query Match 65.2%; Score 947.8; DB 6; Length 1686;
Best Local Similarity 99.8%; Pred. No. 3.9e-182;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 247 tctatgcttccaaatgctgagataaaagttaatctctctcaggattttgagatagtgac 306
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RESULT 12
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LOCUS AX280345 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 80 from Patent WO0177332.
ACCESSION AX280345
VERSION AX280345.1 GI:16607723
KEYWORDS
SOURCE
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (sites)
Mccall,C.A. and Tang,L.
Compositions and methods related to canine igg and canine il-13
receptors
Patent: WO 0177332-A 80 18-OCT-2001;
Heska Corporation (US)
Location/Qualifiers
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ORIGIN

Query Match 65.2%; Score 947.8; DB 6; Length 1686;
Best Local Similarity 99.8%; Pred. No. 3.9e-182;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 4 TCTATGCTTCAAAAGCTCAGATAAAAGTTAATCTCTCAGGATTTTCAGATAGTGAC 63
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QY 307 cctgagatattagggttatctctctttgcaatggcaacctccattattcccgataatttt 366
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QY 427 accatcattaccaagaactctaccataaagaatgggtttgatctcttaacaaaggattgaa 486
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QY 487 gcaagataaaacacactctctgcccagcacaatgcacaaaatggatcagaagttagaagtcca 546
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Db 244 GCAAGATTAACACACTCTTCGCCAGCACAAATGCACAAATGGATGCAGAAATTTAGAACTTCA 303
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RESULT 13
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LOCUS AX280347 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 82 from Patent WO0177332.
ACCESSION AX280347
VERSION AX280347.1 GI:16607725
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 82 18-OCT-2001;
receptors
Heska Corporation (US)
FEATURES
source
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/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 407 a 379 c 388 g 512 t
ORIGIN

Query Match 65.2%; Score 947.8; DB 6; Length 1686;

Best Local Similarity 99.8%; Pred. No. 3.9e-182;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1683 TCTATGCTTTCAATGCTGAGATAAAGATTATCTCTCTCAGGATTTTGAGATAGTGAC 1624
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Db 783 AGTGAGTGAGTGATGAACAATGCTGGAAAGGTGATATCTGGAAGGAAACC 733

RESULT 14
AX280342
LOCUS AX280342 1692 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 77 from Patent WO0177332.
ACCESSION AX280342

VERSION	AX280342.1	GI:16607720
KEYWORDS	dog.	
SOURCE	Canis familiaris	
ORGANISM	Canis familiaris	
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
TITLE	McCall,C.A. and Tang,L.	
JOURNAL	Compositions and methods related to canine igg and canine il-13	
FEATURES	Patent: WO 0177332-A 77 18-OCT-2001;	
source	Heska Corporation (US)	
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BASE COUNT	518 a	376 c 385 g 413 t
ORIGIN		
Query Match	65.2%	Score 947.8; DB 6; Length 1692;
Best Local Similarity	99.8%	Pred. No. 3.9e-182;
Matches 949;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
QY 247	tctatgctttcaaatgctgagataaaagttaaatctctcctcaggattttgagatagtgagac	306
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QY 307	cctggatatttaggttatctctctttgcaatggcaactccattatttcggataaat	366
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64	CCTGGATATTAGGTTATCTCTTTCGATGGCAACTCCATTATTTCCGGATAATTTT	123
QY 367	aaggaatgcacaaatagaaatgaattaaaataccgaacacattgtagtgaacacggaag	426
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124	AAGGAATGCACATAGAAATATGAATTAATAATACCGAAACATTTGATAGTGAAGTGAAG	183
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184	ACCATCATACCAAGAATCTACATTACAAAGATGGGTTTGATCTTAACAAAGGTATTGAA	243
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QY 607	atggactgtgtatattacaactgggcaatatttagctgtctcttggaaacctggcatgggt	666
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364	ATGGACTGTGTATATTACAACATGGCAATATTAGTCTGCTTGGAAACATGGCATGGGT	423
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424	GTCCATTTTGATACCAATTTACCAAGTTGTTTTACTTGGGTATGAGGGCTTGGACCATTCAGCA	483
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Qy 667 gtccattttgataccaattaccagttgttttactgggtatgagggcttgaccattcagca 726
Db 1269 GTCCATTTTGATACCAATTACCAGTTGTTTACTGGTATGAGGGCTTGGACCATTCAGCA 1210
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Db 789 AGTGAGTGGAGTGATGAACAATGCTGGAAGGTGATATCTGGAAGGAAACC 739
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Search completed: September 23, 2002, 15:11:48
Job time: 13201 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:52:01 ; Search time 31.88 Seconds
(without alignments)
2094.606 Million cell updates/sec

Title: US-09-828-995B-61
Perfect score: 2132
Sequence: 1 MAFIHLDVGLYLLVCTAF.....LLKTIFHTKVEFSHQDTFC 386

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_19:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_fodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2132	100.0	386	6	Q95LF0	Q95LF0 canis famil
2	1271.5	59.6	383	11	O88786	O88786 mus musculus
3	572	26.8	404	13	Q90XP8	Q90XP8 oncorhynchu
4	318.5	14.9	427	4	Q96BB4	Q96BB4 homo sapien
5	313	14.7	396	4	Q14631	Q14631 homo sapien
6	312	14.6	420	4	Q14633	Q14633 homo sapien
7	311	14.6	405	6	Q95LF1	Q95LF1 canis famil
8	298	14.0	333	4	Q15469	Q15469 homo sapien
9	297.5	14.0	415	11	Q92OK4	Q92OK4 cavia porce
10	286	13.4	349	6	O97597	O97597 bos taurus
11	283.5	13.3	414	11	Q92058	Q92058 rattus norv
12	272.5	12.8	414	11	O99PS3	O99PS3 rattus norv
13	263	12.3	279	4	O9UDV5	O9UDV5 homo sapien
14	228.5	10.7	343	13	Q9DEQ1	Q9DEQ1 oncorhynchu
15	218.5	10.2	896	11	O64146	O64146 rattus norv
16	199.5	9.4	227	6	Q9GLW3	Q9GLW3 ursus marit

ALIGNMENTS

RESULT 1

Q95LF0 PRELIMINARY; PRT; 386 AA.

ID Q95LF0

AC Q95LF0; 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE INTERLEUKIN 13 RECEPTOR ALPHA CHAIN 2.

GN IL13RA2.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21287533; PubMed=11389954;

RA Tang L.;

RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and alpha2) cDNAs and detection of corresponding mRNAs in canine tissues.";

RT Vet. Immunol. Immunopathol. 79:181-195(2001).

DR EMBL; AF314533; AAL14887.1; -.

KW Receptor.

SQ SEQUENCE 386 AA; 45110 MW; A16FDF2DD023ED95 CRC64;

Query Match 100.0%; Score 2132; DB 6; Length 386;

Best Local Similarity 100.0%; Pred. No. 1.1e-170;

Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 FKECTEYELKRYNIDSENNKTIITKNLHYKDGFDLNGKTEAKINTLLPAQCTNGSEVRS 120

QY 121 SWAETTYTSPQGNRETKIQDMDCVYNNMQYLVCSWKPGMGVHFDNTYQLFYWYEGLDHS 180

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Db 181 AECTDVIKVGKMGCRFPYLESSDYKDFYICVNGSSESQPIRPSYFIFOLQNIKVPMP 240
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Db 241 DYLSLVTKNSEELNKNMMPKGPPIPAKCFIYEIETEDGTTWTTTVENIEQITRTSNES 300
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Db 301 QKICFLVRKSVNTYICSDGDIWSWSDEQCKGDIWKETLVFFLIPAFVIFVLVITCLL 360
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AC O88786;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE IL-13 RECEPTOR ALPHA 2 (INTERLEUKIN 13 RECEPTOR, ALPHA 2).
GN IL13RA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-C3H/HEJ; TISSUE-THYMUS;
RX MEDLINE:98391042; PubMed-9725226;
RA Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,
RA Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,
RA Collins M.;
RT "The murine IL-13 receptor alpha 2: molecular cloning,
RT characterization, and comparison with murine IL-13 receptor alpha 1.";
RL J. Immunol. 161:2317-2324(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U65747; AAC33240.1; -.
DR EMBL; BC003723; AA03723.1; -.
DR HSSP; P16471; 1BP3.
DR MGD; MGI:1277954; IL13ra2.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003532; Hematopo_receptor_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;

Query Match 59.6%; Score 1271.5; DB 11; Length 383;
Best Local Similarity 57.2%; Pred. No. 1.4e-98;
Matches 222; Conservative 71; Mismatches 88; Indels 7; Gaps 3;

QY 1 MAFIHDVGLTLLVCTAFGSMLSNAETKVNPPQDFEIVDPGYGLSLQWQPPFPD 60
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Db 56 FKGCTLEYELKYNVDSDSWKTTITIKNLHYKGFDLNKGIEAKINTLLPAQCTNGSEVR 115
QY 121 SWAETTYWTSPOGNETKIQDMDCVYNNQYLVCSWKPGMGVHFDNYQLFYWYEGLDHS 180
Db 116 PWIEASTGISDEGLSLETKIQDMCKIYNNQYLVCSWKPGTKVTYSDNTYTFWFYEGLDHA 175

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QY 181 AECTDVIKVGKMGCRFPYLESSDYKDFYICVNGSSESQPIRPSYFIFOLQNIKVPMP 240
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QY 241 DYLSLVTKNSEELNKNMMPKGPPIPAKCFIYEIETEDGTTWTTTVENIEQITRTSNES 300
Db 236 EPLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDKNDMKLKRANES 295
QY 301 QKICFLVRKSVNTYICSDGDIWSWSDEQCKGDIWKETLVFFLIPAFVIFVLVITCLL 360
Db 296 EDLCFFVRCKVNTYICADDGIWSESEECWEGYTGPDSKIIFIVPVCLEFFIFULLLCI 355
QY 361 LYKORALLKTIPTHTKKEVFSHQDTFC 386
Db 356 VEKEPEPTLSLHVDLNKEVCAYEDTLC 383

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AC Q90XP8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INTERLEUKIN 13 RECEPTOR ALPHA-2.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Lockyer A.E., Jones C.S., Noble L.R., Verspoor E., Holland J.,
RA Secombes C.J.;
RT "Isolation and characterization of a putative interleukin 13 receptor
RT alpha-2 sequence from rainbow trout (Oncorhynchus mykiss).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF361437; AAL26927.1; -.
KW Receptor.
SQ SEQUENCE 404 AA; 46728 MW; 4B9B7E3F4CFFB6D6 CRC64;

Query Match 26.8%; Score 572; DB 13; Length 404;
Best Local Similarity 32.8%; Pred. No. 6.3e-40;
Matches 105; Conservative 69; Mismatches 142; Indels 4; Gaps 2;

QY 14 LLVCTAFGSMLSNAETKVNPPQDFEIVDPGYGLSLQWQPPFPDNFKECTIEYELKYR 73
Db 13 LMLSDWSQCISKQSEFTVDPDENIGIDDPGLGLPLVIHTAPASLTNLTACSMRYHLEYF 72
QY 74 NIDSENNKTIITIKNLHYKGFDLNKGIEAKINTLLPAQCTNGSEVRSSWAETTYWTSPOG 133
Db 73 NTYQSRWTVIRTVTWYRAQFDLEKEVRVRISTLLGAGCTNGTELKSPETEMVLPNNITG 132
QY 134 NRETKIQDMDCVYNNQYLVCSWKPGMGVHFDNYQLFYWYEGLDHSAECTDYIKVNGKN 193
Db 133 PVSRSVQGGCCVYQKEFHECTWETGLEPTQSQYSLYFHWREMEQAECPQYIHSNGVR 192
QY 194 MGRFPYLESSDYKDFYICVNGSSESQPIRPSYFIFOLQNIKVPMPDYLSLVTKNSEEI 253
Db 193 TGCKFTFEESLSESDENICINSSPEVLRSAFSLQIQNVKPAATETVHLEASPDRL 252
QY 254 NLKNMMPKGPPIPAKCFIYEIETEDGTTWTTTVENIEQITRTSNES-SQKLCFLVRS 309
Db 253 QVQMDLPNERIPRHCLEYEVEAREEGVGQPLQNRVNTMETLTSMDGARRKCFVRS 312
QY 310 KVIYCSDDGIWSEWSDEOC 329
Db 313 RMHYCADRGFWSDWSHWC 332

RESULT 4

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Q96BB4 PRELIMINARY; PRT; 427 AA.

ID Q96BB4 AC Q96BB4

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE INTERLEUKIN 13 RECEPTOR, ALPHA 1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NB NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-COLON ADENOCARCINOMA;

RA Strausberg R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC015768; AAH15768.1; -

KW Receptor.

SQ SEQUENCE 427 AA; 48676 MW; 56A42F7466A39A09 CRC64;

Query Match 14.9%; Score 318.5; DB 4; Length 427;
Best Local Similarity 25.5%; Pred. No. 1.2e-18;
Matches 105; Conservative 64; Mismatches 176; Indels 67; Gaps 19;

QY 11 LYTLLVCTAGSMLSN-AEIKVNPPQDFEIVDPGYGLVSLQWOPPLFPDNFKECTIEYE 69
I : I I I : : : : : : : : : : : : : : : : : :
D 10 LWALLLCAGGGGGAAPTETQPVTNLVSVENLCTVIWTNPP--EGASSNCSLWY- 66

QY 70 LKYRNIDSENKTIITKNLHYKGFDLNKGTEAKINTLL---PAQC-TNGSEYVRSSWAE 124
:
D 67 --FSHFGDKOKKAP-----ETRRSIEVPLNERICLVQSQCSTNESEKPSILVE 115

QY 125 TTYTSPQGNETRIQDMDCVYYNQVLVCSKGMGVHFDNTQLFWYEGLDHSACT 184
:
D 116 KCI-SPEGDGPESAVTELQCIWHNL SYMKCSWLFGRTSPDTNTLYLWHRSLEKIHOCE 174

QY 185 DYIKVGNKMGRPPY--LESSDYKDPIYCVNGSESQIPRPSYFIQOLNIVKMPDPDY 242
:
D 175 NIFR-EQGYFCGSFDLTAKVDSSFEQHSVQIMVKDNAGKIKPSENVLP LTSRVKPDPPHI 233

QY 243 LSLTVKNSSEINKNNPKGPAPKCFIYEIEFTEDGTWTVTTVENEIOITRTSNESQK 302
:
D 234 KNLSFH-NDDLYVQWENPQNFI-SRCFLFYEVFNNS-----QTETHNVFYVQEAACNP 286

QY 303 L-----CFLV-----RSKVNIYC-SDDGIWSESDQCKWDIWKETLV 340
I I I :
D 287 FERNVENTSCFVPGVLPTDLTNTVIRVKTNKLCYEDDKLMSNWSQMSICK---KRNST 343

QY 341 FFLLIPAFVSIFVL-VITCLLLYKORALKTFHTK-----KEVFSHOD 383
:
D 344 LYITMLLIVPVIVAGAIIVLLLYLKR-LKIIFFPIPDPGKIFKEMFGDQN 393

RESULT 5

Q14631 PRELIMINARY; PRT; 396 AA.

ID Q14631 AC Q14631

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR.

GN HSIL5R2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NB NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-PERIPHERAL BLOOD;

RX MEDLINE=9211815; PubMed=1732409;

RT "Molecular cloning and expression of the human interleukin 5

RT "Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;

RT	receptor."	J. Exp. Med.	175:341-351(1992).
DR	EMBL; X61177; CAA43484.1; "		
DR	InterPro; IPR002996; CRIA.		
DR	InterPro; IPR003532; Hematopo_receptor_S_F2.		
DR	PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.		
KW	Signal; Receptor.		
FT	SIGNAL	1	POTENTIAL.
FT	CHAIN	21	396
SQ	SEQUENCE	396 AA; 44998 MW; 1AB60619842ACDA5 CRC64;	
Query Match			
Best Local Similarity 28.9%; Pred. No. 3.1e-18;			
Matches 103; Conservative 62; Mismatches 156; Indels 36; Gaps 15;			
QY	23	MLSAETIKVNPQDFEIVDPCYGLVLSIQWOPPLFPD-NFKECTIETVELKYRNIDSENWK	81
DB	22	LLPDEKISLLPPVNFITKVTG-LAQLVLLQWAPN-PDQEQRVNVEYQVKINARKEDDYE	78
QY	82	TIITKNLHYKDGFDLNGIEAKINTLLPAOCTNGSEVRSSWAETTYTSPGNETRIQD	141
DB	79	TRITES---KCVTILHKGFSASVRTLQ---NDHSLASSWASAEI-HAPGSPGTSIVN	131
QY	142	MDCVYNNQ-----YLVGSKPGMGVHEDTNYQLFYWYEGLDHSAECTDIYK-V	189
DB	132	LTCITNTTETEDNYSRLRSYQVSLHCTWLVTGTDAPETQYFLYYRYG--SWTECOEYSKDT	189
QY	190	NGKNMGCRFP--YLESSDYKDFYICVNGSSSESOPTRPSYFFIQONIVKPMPPDYLSLTV	247
DB	190	LGRNIACWFPPTFILSKGRDMLAVLVNGSSKHSARPPDQFLAHAIQIINPP--LNVTA	247
QY	248	K-NSEETLNKNMKGPIPAKCFIYEIEF--TEDGTTWTTTVE--IQITFTSNESOKL	303
DB	248	EIEGTRLSIQEWKPVSAFFIHCDFYEVKIHNRNGYLQIEKLMTNAFISII---DDLKY	304
QY	304	CFLVRKNNIYCSDDGIWSENSDQCGKGTWKETLVFLFPFAPVSVFLVITCLL	360
DB	305	DVQVRAVSSVSCREAGLWSEWSQPIYGVNDEHKPLREWFVIVIMATIFICILLISLI	361
RESULT 6			
Q14633	PRELIMINARY;	PRT;	420 AA.
ID	Q14633		
AC	Q14633;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	INTERLEUKIN-5 RECEPTOR PRECURSOR.		
GN	HSIL5R.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PERIPHERAL BLOOD;		
RC	MEDLINE=92121815; PubMed=1732409;		
RA	Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;		
RT	"Molecular cloning and expression of the human interleukin 5		
RT	receptor.";		
RL	J. Exp. Med. 175:341-351(1992).		
RL	EMBL; X61176; CAA43483.1; "		
DR	InterPro; IPR002996; CRIA.		
DR	InterPro; IPR003532; Hematopo_receptor_S_F2.		
DR	PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.		
KW	Signal; Receptor.		
FT	SIGNAL	1	POTENTIAL.
FT	CHAIN	21	420
SQ	SEQUENCE	420 AA; 47670 MW; 8DC56DFC8BEFF524 CRC64;	
Query Match			
Query Match			
Best Local Similarity 14.6%; Score 312; DB 4; Length 420;			
Matches 103; Conservative 62; Mismatches 156; Indels 36; Gaps 15;			

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Best Local Similarity 28.6%; Pred. No. 4e-18;
Matches 102; Conservative 63; Mismatches 156; Indels 36; Gaps 15;

QY 23 MLSNAEIKVNPQDFEIVDPGVLGYLSLQWQPPD-NFKECTIEYELKYRNIDSENWK 81
DB 22 LLPDEKISLPPVNFITKVTG-LAQVLLQWKPN--PDQQRNVNLEYQVKINAPKEDDYE 78
QY 82 TITIKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSVRSWAETTVTSPQGNRETKIOD 141
DB 79 TRITES---KCVTILHKGSASVRTILQ---NDHSLASSWASAEI-HAPPGSPGTSVNV 131
QY 142 MDCVYVNWQ-----YLVCSWKPGMGVHFDNYQLFYWYEGLDHSAECTDIK-V 189
DB 132 LTCTNTTNTEDNYSRLRSYQVSLHCTWLVTGDPEDQYFLYRYG--SWTECQEQYSKDT 189
QY 190 NKGKMGCRPP--YLESSDYKDFYICVNGSSEOPRPSYFIFOLQNVKPMPPDYLSLTV 247
DB 190 LGRIACWFPRIILSKGRDWLAVLVNGSSKHSARPPDOLFALHAIDQINPP--LNVTA 247
QY 248 K-NSEINLKNWPKGPIPAKCFIYEIEF--TEDGTTWTTTVEINE-IOITRTSNESQKL 303
DB 248 EIEGTRLSIQWEKPVSAFFPHCFDYEKIHNTNRNGYLOIEKLTNAFISII---DDLSKY 304
QY 304 CFLVRSKVNIIYSDGDIWSEWSEQWCKDIWKTILVFLIPFAFVSIFVLVITCLL 360
DB 305 DVQVRAAVSSMCREAGLWSEWSPQIVVGNDEHKPLREWFVIVIMATICPILLILSLI 361

RESULT 7
Q95LF1 PRELIMINARY; PRT; 405 AA.
AC Q95LF1;
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE INTERLEUKIN 13 RECEPTOR ALPHA CHAIN 1 (FRAGMENT).
GN IL13RAL.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21287533; PubMed=11389954;
RA Tang L.;
RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and
RT alpha2) cDNAs and detection of corresponding mRNAs in canine
RT tissues."
RL Vet. Immunol. Immunopathol. 79:181-195(2001).
DR EMBL; AF314532; AAL14886.1; -.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 405 AA; 46328 MW; 926E1AC7BE5E3F42 CRC64;

Query Match 14.6%; Score 311; DB 6; Length 405;
Best Local Similarity 26.8%; Pred. No. 4.7e-18;
Matches 97; Conservative 59; Mismatches 156; Indels 50; Gaps 17;

QY 52 WQPPLEPDPNFKECTIEYELKYRNIDSENWKTIITKNLHYKDGFDLNGKIEAKINTLLPAQ 111
DB 30 WAPP--EGASPNCTRLY---FHFQDNKQDKIAPET-HRSKEVPLNERICLQVG----SQ 79
QY 112 C-TNGSEVRSSNAETTYTSPQGNRETKIODMDCVYVNWQYLVCSWKPGMGVHFDNYQL 170
DB 80 CSTNESDNPISILVEKC-TPPPEGDPESAETVLCQVWHNLSYMKCTWLPGRNTSPDNTYL 138
QY 171 FYWYEGLDHSAECTDIKYVNGKMGCRFPY--LESSDYKDFYICVNGSSEOPRPSYF 228
DB 139 YVWHSSLGKILQCEDIYR-EGQHIGCSFALTNLKDSFQHSQVQIMVKDNARKIRSFNI 197
QY 229 FOLQNTVKNPMPDYLSLTVKNSEINLKNWPKGPIPAKCFIYEIEFTEDGTTWTTTVE 288
DB 305 DVQVRAAVSSMCREAGLWSEWSPQIVVGNDEHKPLREWFVIVIMATICPILLILSLI 361
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DB 198 VPLTSHVKDPDPHIKRLFPQNG-NLYVQWKPNQ-FYSRCLSVQVEVNNSTQETNDFYV 255
QY 289 NELIQTRTNSQO---KLCFLV-----RSKNVIYC-SDDGIIWSEWSDQCHWK 331
DB 256 EBAKQNSFEQNEGLECTICFMVPGVLPDLTNTVIRVTRTKLCYEDDKLWNSMQAM--- 312
QY 332 GDIMWETLVFFIIPFAFVSIFVL--VITCLLLYKORALLKTIFFHTK-----KEVFES 381
DB 313 -SIGENTDFTFYITMLLATQVIVAGAIILLLYLKR--LKIIFFPIPDGKIFKEMFGD 369
QY 382 QD 383
DB 370 QN 371

RESULT 8
Q15469 PRELIMINARY; PRT; 333 AA.
AC Q15469;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
GN HSIL5R4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=PERIPHERAL BLOOD; PubMed=1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tomimaga A., Takatsu K.;
RT "Molecular cloning and expression of the human interleukin 5
RT receptor."
RL J. Exp. Med. 175:341-351(1992).
DR EMBL; X62156; CAA44081.1; -.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003532; Hematopo_receptor_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.
SQ SEQUENCE 333 AA; 37722 MW; 8D9239845E16985B CRC64;

Query Match 14.0%; Score 298; DB 4; Length 333;
Best Local Similarity 29.5%; Pred. No. 4.6e-17;
Matches 95; Conservative 57; Mismatches 134; Indels 36; Gaps 15;

QY 23 MLSNAEIKVNPQDFEIVDPGVLGYLSLQWQPPD-NFKECTIEYELKYRNIDSENWK 81
DB 22 LLPDEKISLPPVNFITKVTG-LAQVLLQWKPN--PDQQRNVNLEYQVKINAPKEDDYE 78
QY 82 TITIKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSVRSWAETTVTSPQGNRETKIOD 141
DB 79 TRITES---KCVTILHKGSASVRTILQ---NDHSLASSWASAEI-HAPPGSPGTSIVN 131
QY 142 MDCVYVNWQ-----YLVCSWKPGMGVHFDNYQLFYWYEGLDHSAECTDIK-V 189
DB 132 LTCTNTTNTEDNYSRLRSYQVSLHCTWLVTGDPEDQYFLYRYG--SWTECQEQYSKDT 189
QY 190 NKGKMGCRPP--YLESSDYKDFYICVNGSSEOPRPSYFIFOLQNVKPMPPDYLSLTV 247
DB 190 LGRIACWFPRIILSKGRDWLAVLVNGSSKHSARPPDOLFALHAIDQINPP--LNVTA 247
QY 248 K-NSEINLKNWPKGPIPAKCFIYEIEF--TEDGTTWTTTVEINE-IOITRTSNESQKL 303
DB 248 EIEGTRLSIQWEKPVSAFFPHCFDYEKIHNTNRNGYLOIEKLTNAFISII---DDLSKY 304
QY 304 CFLVRSKVNIIYSDGDIWSEWSPQIVVGNDEHKPLREWFVIVIMATICPILLILSLI 361
DB 305 DVQVRAAVSSMCREAGLWSEWSPQIVVGNDEHKPLREWFVIVIMATICPILLILSLI 361
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:51:31 ; Search time 21 Seconds
(without alignments)
1766.213 Million cell updates/sec

Title: US-09-828-995B-61
Perfect score: 2132
Sequence: 1 MAFIHLDVGFLLVLCVAF.....LLKTIHTKKEVFESHQDTFC 386
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	349.5	16.4	426	2 JC7773	IL-13ralpha 1 prot
2	312	14.6	420	2 S21052	interleukin-5 rece
3	298	14.0	335	2 A40267	interleukin-5 rece
4	266	12.5	415	2 S12357	interleukin-5 rece
5	256	12.0	831	2 J01655	prolactin receptor
6	232	10.9	369	2 A42565	interleukin-2 rece
7	221	10.4	878	1 A40091	interleukin-3 rece
8	221	10.4	896	1 A35782	cytokine receptor
9	218.5	10.2	896	2 I56563	interleukin-3 rece
10	217.5	10.2	830	2 I50455	prolactin receptor
11	216	10.1	373	2 A55718	interleukin-2 rece
12	208	9.8	369	2 I49280	interleukin-2 rece
13	195	9.1	581	2 I45971	prolactin receptor
14	194	9.1	310	2 A29884	prolactin receptor
15	194	9.1	412	2 A41070	prolactin receptor
16	194	9.1	610	2 A36116	prolactin receptor
17	193	9.1	610	2 A34631	lactogen receptor
18	192	9.0	897	1 A39255	cytokine receptor
19	189	8.9	292	2 I77525	prolactin receptor
20	189	8.9	303	2 I77524	prolactin receptor
21	189	8.9	608	2 I53269	prolactin receptor
22	180.5	8.5	630	2 I51086	prolactin receptor
23	178	8.3	616	2 A30304	prolactin receptor
24	172.5	8.1	288	2 B59405	prolactin receptor
25	172.5	8.1	376	2 A59405	prolactin receptor
26	172.5	8.1	622	2 A40144	prolactin receptor
27	154.5	7.2	917	2 I49699	glycoprotein 130 -
28	150	7.0	918	2 A36337	membrane glycoprot
29	145	6.8	918	2 A44257	interleukin-6 sign

30 144.5 6.8 400 2 S06945 granulocyte-macrop
31 143 6.7 333 2 S13684 granulocyte-macrop
32 143 6.7 378 2 S50040 granulocyte-macrop
33 136.5 6.4 638 2 S12136 somatotropin rece
34 131.5 6.2 378 2 A40266 interleukin-3 rece
35 130 6.1 150 2 B34631 lactogen receptor
36 127.5 6.0 638 2 B28176 somatotropin rece
37 127.5 6.0 800 1 S31575 interleukin-4 rece
38 127.5 6.0 1557 2 D41214 protein-tyrosine-p
39 127.5 6.0 1630 2 C41214 protein-tyrosine-p
40 127 6.0 286 2 S50039 granulocyte-macrop
41 124.5 5.8 1097 2 S17308 leukemia inhibitor
42 123.5 5.8 817 2 A48721 titin, muscle - ch
43 123 5.8 825 1 A60386 interleukin-4 rece
44 122.5 5.7 1825 2 C88400 protein H19M22.1 l
45 122.5 5.7 1825 2 T32828 hypothetical prote

ALIGNMENTS

RESULT 1
JC7773
IL-13Ralpha 1 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: JC7773
R:Pierrot, C.; Beniguel, L.; Beque, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:Title: Expression of a functional IL-13Ralpha by rat B cells.
A:Reference number: JC7773; PMID:11573960
A:Accession: JC7773
A:Molecule type: mRNA
A:Residues: 1-426 <PIE>
A:Cross-references: CB:AY044251
C:Comment: This protein is an functionally binding protein involved in B cell prolif
C:Genetics:
A:Gene: il-13ralpha

Query Match	16.4%	Score 349.5;	DB 2;	Length 426;
Best Local Similarity	27.9%	Pred. No. 3.7e-19;		
Matches 113;	Conservative	65;	Mismatches 178;	Indels 49;
Gaps	18;			
Qy	10	FLYTLVCTAFGSLMSNAEI--KVNPPQDFEIVDPGYLGYLISLQWQPLFPDNEKECTIE	67	
Db	6	WLGELLVLLFAASLDQVALATEVQPPVTNLSVSVENLCTIVTWTWSP--EGASPNCSLR	63	
Qy	68	YELKYRNIDSENWKTITTKNLHYKGFDLNKGIEAKINTLLPAQC-TNGSEVRSSWAETT	126	
Db	64	Y---FSHFDDQDKKIAPETRRKKE-LPLNE----KICLVGSGCSTNESEKPSPLVKKC	115	
Qy	127	WYTSPOGNRETKIODMDCVYVYVWQVLCVSWKPGMGVHEDTNVQLFYWYEGLDHSAECTDY	186	
Db	116	I-SPRRGSESAVTELOCTWHNLSYMKCSWLPKGNWTSPTNTYLYWYSSGLSKSLQC-EN	173	
Qy	187	IKVCKNKGCRFPYLE-SSDYKDFYICVNGSSESOPRPSYFIFOLQIVKPMPPDYLSL	245	
Db	174	IHRGQIHGCSFKLTKVESNYEHNNIQLMVKNAGKIRPSYKIVSFTSNVRPGPHIKHL	233	
Qy	246	TVKNSSEINLKNWPKGPPIAKCFIYEIEFTDGT-TWTTTVEINEIQTITSNESQKL-	303	
Db	234	FLKNG-ALFVQWKPNQ-N-FSSRCLSYEVEVNSTQDTSYNSNSLEVEEDKCNSEFDRNNE	291	
Qy	304	---CFL-----VRSKVNIIYCSDDG-IWSEWSDQCWKGDITWKE-TLVFFFLIP	345	
Db	292	GASCFISPGVLXNTVYTVRVKTNKLCFDDNDLMSNNSEAL----SIGKEPNSTFTYTM	347	
Qy	346	FAFYISFVLVITCLLYKQKRALTKTIF-----HTKKEVFESHQD	383	
Db	348	LLIIPFVAVVAVIIILLFYLKRLKIIIFPPIDPGKIFKFMFGDQN	392	

A:Cross-references: GB:D90205; NID:g220465; PIDN:BAAL4231.1; PID:g220466
C:Keywords: cytokine receptor; transmembrane protein

Query Match 12.5%; Score 266; DB 2; Length 415;
Best Local Similarity 25.7%; Pred. No. 8.6e-13;
Matches 95; Conservative 71; Mismatches 166; Indels 38; Gaps 17;
Qy 8 VGFLTLVCTAFGSLNAEIKVNPQDFEIVDPGYLGYSLOWQPPLPDP-NFEKCTI 66
Db 9 VGALATLQ-----ADLNHKKFLLPPVNFITKATG-LAQLVLLHNDP--PQOEORHVDL 60
Qy 67 EYELKYRIDSNNKWTITKNIHYKDGFDLNGIDIAKINTLLPAOCTGSEVRSSWAET 126
Db 61 EYHVINAPQDEYDTRKTES---KCVTPLHEGFAASVRTILKSSHTT---LASSWSAE 114
Qy 127 YWTSPOGNETKIQDMDCVYNN-----WQY-LVCSWKPGMGVHFDTNVQLFYWE 175
Db 115 L-KAPGSGPSTVTLCTTHVWSSHTLHPYQVSLRCTWLVGKDAPEDTOYFLYIRFG 173
Qy 176 GLDHSACTDYIK-VNGKNMGRFP--YLESSDYKDFYICVNGSSSESQPIRPSYEFQIQ 232
Db 174 VL--TEKCOEYSRDALNRNTACWFFRTFINSKGFQOLAVHINGSKRAAIKFPDQLFSL 231
Qy 233 NIVKPMPPDYLSLTVKNSEELNKNMKGPIPAKCFIYEIEF--TEDGTTWTTTVE 290
Db 232 AIDQVNPRTNVTVEIE-SNSLYIOWEKLPLSAPPDCHFNVELKIYNTKNGHIQEKLIANK 290
Qy 291 IQITRTSNESOKLFLVRSKVNIIYSDGIGWSEWDEQCWKGDWKETLVFFLIPAFVS 350
Db 291 F-ISKIDVVS-TYSTQVRAAVSSPCMPGRNGEWS-QPIYVGKRSKLVEWHLIVLPTAA 347
Qy 351 IFVLVITCLL 360
Db 348 CFVLLIFSLLI 357

RESULT 5
QJ01655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
A:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se
A:Reference number: JQ1655; MUID:93075121
A:Accession: JQ1655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAAO2439.1; PID:g222849
A:Experimental source: kidney
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAP>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:236-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (coval

Query Match 12.0%; Score 256; DB 2; Length 831;
Best Local Similarity 25.4%; Pred. No. 1.2e-11;
Matches 100; Conservative 58; Mismatches 161; Indels 74; Gaps 19;
Qy 15 LVCTAFGSLNAEIKVNPQDFE---IVDPG-----YLGYSLQWQPPPLFP 58
Db 101 ITVTATNEIGNS-----SDPQVVDVTSIVQPGSPVNLTLTKRSANIMYLWAKWSPPLLA 156
Qy 59 DNFKECTIEYELKYRNIDSENKWTITKNIHYKDGFDLNGKIEAKINTL-----LPAQ 111
Db 157 DASSNHLHYELRIKPEKEETI-----SVGVQVQCKINRLNAGMYVQVR 205

Qy 112 CTNGSEVRSSWAETTYTWTSPQG-NRETKIQDMDCVYNNWQYLVCSWKPGMGVHFDTNYL 170
Db 206 CTLDPCGEWSESSERHILIPSGSPPEKPTTIKRSPEKETFTCMWPKGLDGGHPTNYTL 265
Qy 171 FWYEGLDHSACTDYIKVNGKNMGRFPYLESSDYKDFYICVNGSSE--SQPIRPSYFI 228
Db 266 LYSKEGEOVYECPPY-RTAGPN-SCYFDKKHTSEWTIYNTITVRATNMGSSNDPHY-- 321
Qy 229 FOLQNVKPMPPDYLSLTVKNSEELN-----LKNMP-----KGPIAKCFIYEIEF- 275
Db 322 VDVTVIVQDPP--VNVTLLELKRPNRKPYLVLTWSPPLADVRSGLWLTLE---YELRLK 376
Qy 276 TEDGTTWTTTVEIEIQITRTS-NESOKLFLVRSKVNIIYCSDD--GIWSEWDEQCWK- 331
Db 377 PEEGEWETIFVGQQTQYKMFSLNPKKYI-----IQHCKPDHHGSWSEWSSENYIQI 430
Qy 332 -GDIWKETLVFFLIPAFVSIFVLVITCLLLYK 363
Db 431 PNDFRVKDMIVWILVGLVSLCLINSWTMVLK 463

RESULT 6
A42565
interleukin-2 receptor gamma chain - human
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
A:Accession: A42565; A46591; I54332
R:Takeishi, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.
Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; MUID:92335883
A:Accession: A42565
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <TAK>
A:Cross-references: GB:D11086; NID:g303611; PIDN:BAAO1857.1; PID:g219890
A:Experimental source: MOLT beta lymphoid cells
A:Note: sequence extracted from NCBI backbone (NCBIP:109167)
R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; MUID:93293887
A:Accession: A46591
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:g307058
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.;
Hum. Mol. Genet. 2, 1099-1104, 1993
A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-11
A:Reference number: I54332; MUID:94004847
A:Accession: I54332
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:L19546; NID:g349631; PIDN:AAC37524.1; PID:g349632
C:Genetics:
A:Gene: GDB:IL2RG; SCIDX1; IMD4
A:Cross-references: GDB:I34807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A:Note: defects are associated with an X-linked form of severe combined immunodeficie
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunod

Query Match 10.9%; Score 232; DB 2; Length 369;
Best Local Similarity 24.1%; Pred. No. 2.9e-10;
Matches 65; Conservative 48; Mismatches 123; Indels 34; Gaps 9;
Qy 125 TTYTSPQGNRET-----KIQDMDCVYNNWQYLVCSWKPGMGVHFD 165
Db 125 TTYTSPQGNRET-----KIQDMDCVYNNWQYLVCSWKPGMGVHFD 165

Db 25 TWTILT-PNGNEDTTADFLTMTPTDLSYSTLPLPEVQCFVFNVEYMNCTWNSSEPO-P 82
QY 166 TNYQLFYWYEGDHS--AECTDYIKVNGKNMGCRPPYLESSDYKDFYICVNGSSSQPTR 223
Db 83 TNLTLHYWYKNSDNKVKQSHYLFSEERTSCQLOKKEIHLYQTFVVLQDPRE--PRR 140
QY 224 PSYFIQQLQNIYKPPHPPDLSYLVTKNSBEINLKNWMPGPIPAKCFIYVEIETED-GTWM 282
Db 141 QATQMLKQLNLVWPAPENLTLKLSQLELNN--NRFNLHGLEHLVQVYRTDWDHSH 197
QY 283 VTTTVEIETQITRTSNESOK-LCFVLRKVNITYCSDGIGWSEWSDEQCKGDIWKETLVF 341
Db 198 TEQSDVDYRHKFLSPVDQGRYTFVRFRNPLCGSAQWSEWSHPHNGSNTSKENPFL 257
QY 342 FLIPEAFVSI----FVLVITCLLYKQAL 367
Db 258 FALEAVTISVSGMGLIISLLCYFWLERTM 287
RESULT 7
A40091
Interleukin-3 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A40091; A43022
R:Itoh, N.; Yonehara, S.; Schreurs, J.; Gorman, D.M.; Maruyama, K.; Ishii, A.; Yahara, I.
Science 247, 324-327, 1990
A:Title: Cloning of an interleukin-3 receptor gene: a member of a distinct receptor gene
A:Reference number: A40091; MUID:90117145
A:Accession: A40091
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-878 <I>Q>
R:Gorman, D.M.
submitted to GenBank, November 1989
A:Reference number: A43022
A:Accession: A43022
A:Molecule type: mRNA
A:Residues: 1-815,'Q',817-878 <GOR>
C:Cross-references: GB:M29855; NID:g198342; PIDN:AAA39295.1; PID:g309406
C:Comment: In mice there are two classes of high-affinity IL-3 receptors. One contains
receptors.
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor; duplication; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-878/Product: interleukin-3 receptor beta chain #status predicted <MAT>
F:23-440/Domain: extracellular #status predicted <EXT>
F:39-236/Domain: cytokine receptor homology <CRS1>
F:254-433/Domain: cytokine receptor homology <CRS2>
F:441-462/Domain: transmembrane #status predicted <TMM>
F:463-878/Domain: intracellular #status predicted <INT>
Query Match 10.4%; Score 221; DB 1; Length 878;
Best Local Similarity 24.5%; Pred. No. 6e-09;
Matches 86; Conservative 58; Mismatches 155; Indels 52; Gaps 19;
QY 33 PPQDFEIVDPGVGLVSLQWQPLFPDN--FKECTIEYELKYNIDSENWKTITTKNLH 89
Db 139 PKPDTHISPSG--DHFLLEWSVSLGDSQVSWLSSDKDIEFVAYKRL-QDSWED--ASSLH 193
QY 90 KYDGFDLNKGIBAKI---NTLLPA----QCTNGSEVR---SSWAETTYWTSPQGNRETKI 139
Db 194 -TSNQVN--LEPKFLPNSIYAARVTRLSAGSSLSGRPSRWSPEVHWDSPGDK-AQP 249
QY 140 QMDCVYNNQWLVCSWPKGCVGHEDTNYQLFYWYEGDLHSAECTDYIKVNGKNM----G 195
Db 250 QNLQCFDFGDIQSLHCSWEVWTTQTTGSVFGFLYRPSPAAPEKCSPPVVKPEQASVYTRYR 309
QY 196 CRFPYLESSDYKDFYICVNGSSSQPTRPSYFIQQLNIYKPPHPPDLSYLVTKNSSEINL 255
Db 310 CSLPVPERSAHSQYIVSVKHLQGGKFIWSYHI-----QMEPILNQ-T-KNRDSYSL 360

QY 256 KWNMPKGPPIAKC-FIYEIEFTEDGTWTTTVEIETQITRTS-----NESQKLCFLVRSK 310
Db 361 HWETQK--IPKYIDHTFQVQYKKSKESWKDKSTENLGRVNSMDLPQLEPDTSYCARVRVK 418
QY 311 -VNIYCSDDGISEWSDEQCKGDIWKETLVFLFPFAPVSIYFVLVITCLL 360
Db 419 PTSDY---DGIWSEWSNEVWTTDWMPTLWILVI-----LVFLIFTLLL 460
RESULT 8
A35782
cytokine receptor common beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A35782
R:Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Arai, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A:Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like pro
tein
A:Reference number: A35782; MUID:90319131
A:Accession: A35782
A:Molecule type: mRNA
A:Residues: 1-896 <GOR>
A:Cross-references: GB:M34397; NID:g191821; PIDN:AAA37204.1; PID:g309101
C:Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 rece
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor; duplication; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-896/Product: cytokine receptor common beta chain #status predicted <MAT>
F:23-441/Domain: extracellular #status predicted <EXT>
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-434/Domain: cytokine receptor homology <CRS2>
F:442-463/Domain: transmembrane #status predicted <TMM>
F:464-896/Domain: intracellular #status predicted <INT>
Query Match 10.4%; Score 221; DB 1; Length 896;
Best Local Similarity 22.6%; Pred. No. 6.1e-09;
Matches 90; Conservative 64; Mismatches 153; Indels 92; Gaps 21;
QY 31 VNPPQDFEIVDPGVGLY-----LSLQWQPLFPDN----- 60
Db 100 VPIYTRFSTNEDYSFRPDSDLGLQMLVLAQNVQPPPL-PKNVISSESDRFLLEWSVS 158
QY 61 -----FKECTIEYELKYNIDSENWKTITTKNLHYKDGFDLNKGIEAKI----- 104
Db 159 LGDAQVSWLSSDKDIEFVAYKRL-QDSWED--AYSILH-TSKFQVN--PEPKFLPNSIYA 212
QY 105 ----NTLLPAQCTNGSEVRSSWAETTYWTSPQGNRETKIQDMDCVYNNQWLVCSWPKGM 160
Db 213 PRVTRLYPGSSLSGRP--SRWSPEAHWDSPGDK-AQPQLQCFDFGDIQSLHCSWEVWT 269
QY 161 GVHFDNTYOLFVWYEGDLHSAECTDYIK-VNGKNM----GCRFPYLESSDYKDFYICVNG 215
Db 270 QTTGSVSGFLYRPSVPAPEKCSPPVVKPEPPGASVTRYHCSLPVPEPSAHSQYITVSVKH 329
QY 216 SSESQPIRPSYFIQQLNIYKPPHPPDLSYLVTKNSBEINLKNWMPGPIPAKCFI---YE 272
Db 330 LQGGK-----FIMSYNHI--QMEPTLNT-KNRDSYSLHWETQK---MAYSFIEHTTQ 377
QY 273 IEFTEDGTWTTTVEIETQITRTSNESQ---KLCFLVRKVNITYCSDGIGISEWSDEQC 329
Db 378 VOYKKKSDSWEDSKTEN-LDRAHSMDSLSQLEPDTSYCARVRVKPISNYDGIWSEVYT 436
QY 330 WKGD-----IWKETLVFLFPFAPVSIYFVLVITCLLYK 363
Db 437 WKTDMWMPPLWILVILVFLI---LTLILLRFGCVSVYR 472
RESULT 9
I56563
interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999

C:Accession: I56563
R:Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and
A:Reference number: I56563; MUID:95370942
A:Accession: I56563
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
C:Genetics:
A:Gene: rIL-3Rbeta
C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-433/Domain: cytokine receptor homology <CRS2>

Query Match 10.2%; Score 218.5; DB 2; Length 896;
Best Local Similarity 22.0%; Pred. No. 9.5e-09;
Matches 81; Conservative 60; Mismatches 154; Indels 73; Gaps 16;

Qy 33 PPQDFEIVDPVGLVSLQWOPPLFPDN---FKECTIEYELKYRNIDSENKTIITKNLH 89
Db 138 PKKDISPSFG--DHFLKWSVPLGDAQVSLLSOKDIQFEVAYKOL-QDSWED--ASSLH 192
Qy 90 YKQDFDLNKGIEAKINTLLP-----AQCTNGSEVR---SSWAETTYWTSPOGNET 137
Db 193 -----TCNLWLTLEPKLPNSIYVARVRAQLAPGSSLSGRPSGWSPEVHSDSPEDK-A 246
Qy 138 KIQMDCVYVNOYLVCWSKPGMGVHFDNTYOLFVWYEGLDHSAECTDYIKVNGKMGCR 197
Db 247 RPQNLQCFDFGQSLNCSWEVMTKVTDSVSGFLFYSSSPKAGEKKCSPPWK----- 297
Qy 198 FPYLESSDYKDFYICVNGSSSEOPRPSYFFIFOLQNIYK-----PWPPDYLSLTV 247
Db 298 --ELQASATRYTHCSLN---VSDPAHSQYTVSVKRLQGGKFIESFNHIQNPPLNLT- 351
Qy 248 KNSEINLKNWPKGPIPAKCFIYIEFTEDGTTWTTTVEINEIQITRTSNESOKL----- 303
Db 352 KNRSYSLHWETQKMSYFFIOHAFQVQYKKLDRWEDSKTEN-----LNHSHMDLPQ 404
Qy 304 -----CFLVRSKVNIYSDGIGWSWSEDCQWKGD-----IW-KETLVFFLIPFAVSI 352
Db 405 LEPGTSYCARVRVKTIPEYKGLSEWSNNECTWTTDWMPTLWILVILFLITLFLALLRF 464
Qy 353 VLVITCLL 360
Db 465 GCIVGCKL 472

RESULT 10
150455
prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
A:Accession: I50455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A:Reference number: I50455; MUID:94283267
A:Accession: I50455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CH>
A:Cross-references: EMBL:U07694; NID:9466381; PIDN:AAA20646.1; PID:9466382
C:Superfamily: cytokine receptor homology
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 10.2%; Score 217.5; DB 2; Length 830;
Best Local Similarity 25.7%; Pred. No. 1e-08;

Matches 87; Conservative 53; Mismatches 158; Indels 41; Gaps 16;

Qy 47 YLSLQWOPPLPDNFKECTI-EYELKYRNIDSENKTIITKNLHYKDGFDLKNKGIEAKIN 105
Db 145 YLLAKWSPPPLADVTSNSHVRYELRLKPEEKEWETV---SVGQVQYKYNR-LQAGVK 200
Qy 106 TLLPAQCTNGSEVRSSWAETTYWTSPOG-NRETKIQDMDCVYVNOYLVCWSKPGMGVHF 164
Db 201 YVQVRCVLDITGEWSEWSESRHHIPNGESPPEKPTIIFKCRSPKETTTTCMMKPGSDGGH 260
Qy 165 DTNYOLFVWYEGLDHSAECTDYIKVNGKMGCRFFPYLESSDYKDFYICVN-----GSSES 219
Db 261 PTNLTLLSKGEERVYECPDY-KTAGPN-SCYFDKKHTSFWTIYINIVKATNEIGSNVS 318
Qy 220 QPIRPSYFIFOLQNIYKMPDPDYLSL---TVKNSEELKNWMPKGPIPA-----KCFI 270
Db 319 DPL-----YVDVTYIVQTDPPVNVTLKKTIVNRKPVLVLTWSPD--PLADVRSGLTLD 371
Qy 271 YEIEF-TEDGTTWTTTVEINEIQITRTS-NESQKLCFLVRSKVNIYCSDD--GIWSEWSD 326
Db 372 YELRLKPEEAEWETIFVGQOQTHYKMFSLNPGKKYI-----VQIHCKPDHHGSWSEWS 425
Qy 327 EQCKK--GDIWKETLVFFLIPFAVSIFFVLITCLLLYK 363
Db 426 EKYIQIPTDFRIKDMVWVWIIIGVLSLCLVNSWTWMLK 464

RESULT 11
A55718
interleukin-2 receptor gamma chain precursor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
A:Accession: A55718
R:Henthorn, P.S.; Somborg, R.L.; Elmiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg
Genomics 23, 69-74, 1994
A:Title: IL-2/gamma gene microdeletion demonstrates that canine X-linked severe combi
A:Reference number: A55718; MUID:95130114
A:Accession: A55718
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373 <HN>
A:Cross-references: GB:U04361; NID:g517411; PIDN:AAC48403.1; PID:g517412
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication

Query Match 10.1%; Score 216; DB 2; Length 373;
Best Local Similarity 25.1%; Pred. No. 5e-09;
Matches 70; Conservative 51; Mismatches 128; Indels 30; Gaps 11;

Qy 104 INTLLPAQCTNGSE-----VRSSWAETTYWTSPOGNETKIQDMDCVYVNOYLVCWS 156
Db 23 LNSTVP--MPNGNEDITPDFFLTATPSETLSVSS-----LPLEVQCFVFNVEYMNCTW 74
Qy 157 KPGMGVHFDNTYQVFWYEGE--DHSABCTDYIKVNGKMGCRFFPYLESSDYKDFYICVN 214
Db 75 NSSSEPR-PTNLTLLHYWYKNSNDKQVQECGHYLSREVTAAGCWLQKEETHLYETFEVQLR 133
Qy 215 GSSESQPIRPSYFFIFOLQNIYKMPDPDYLSTLVKNSEELKNWMPKGPPIPAKCFIYEIE 274
Db 134 DPRE--PRRQSTQKLUKLQNLVPAWAPENLTLHNLSESLSELSWS---NRHLDHCLHVVQ 188
Qy 275 FTED-GTTWTTTVEINEIQITRTSNESOKL-CFLVRSKVNIYCSDDGIWSEWSEDCQWK 332
Db 189 YRSDWDRSWTQSDVDRNSFSPLPSVDGQKFTYFRVRSYRNPLCCGSAQRWSEWSHPHIGHS 248
Qy 333 DIWKETLVF-----FLIPFAVSIFFVLITCLLLYKQRAL 367
Db 249 NTSKENPLFASEAVLPLGSMGLIISLI-CVYYWLERSI 286

RESULT 12
149280

interleukin-2 receptor gamma chain precursor - mouse

C:Species: Mus musculus (house mouse)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
R:Cao, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gamma chain
A:Reference number: A47514; MUID:93391374
A:Accession: I49280
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <CAO>
A:Cross-references: EMBL:U01795; NID:g727349; PIDN:AAA64279.1; PID:g727350
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:L20048; NID:g404067; PIDN:AAA93286.1; PID:g404068
R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of function
A:Reference number: JN0592; MUID:93277575
A:Accession: JN0592
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <KUN>
A:Cross-references: DBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:g303685
R: Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A:Reference number: JN0775; MUID:93366191
A:Accession: JN0775
A:Molecule type: mRNA
A:Residues: 1-369 <KOB>
A:Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046
R:Chiu, R.K.; Dougherty, G.J.
submitted to the EMBL Data Library, October 1993
A:Description: Regulation of CD44-mediated cellular adhesion by the IL-2 R gamma chain.
A:Reference number: S37582
A:Accession: S37582
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
A:Cross-references: EMBL:X75337
R:DiSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
Eur. J. Immunol. 24, 3014-3018, 1994
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal location
A:Reference number: I53398; MUID:95104285
A:Accession: I53398
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555
C:Genetics:
A:Gene: IL-2rgamma
A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), beta (see PIR:UHMS2), and gamma (see PIR:UHMS2) subunits.
C:Function:
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK cells
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
F:256-284/Domain: transmembrane #status predicted <TM>
F:71-75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 9.8%; Score 208; DB 2; Length 369;
Best Local Similarity 23.4%; Pred. No. 2e-08;
Matches 64; Conservative 50; Mismatches 121; Indels 38; Gaps 10;

QY 118 VRSSWAETTYTWTSPGNETK-----IODMDCVYVYNWOYLVCWSKP 158
DB 19 LRAGSSKVLMS--ANEDIKADLILSTAPHELSAPTLPPEVOCFVFNIMYMTWNS 76
QY 159 GMGVHFDNNYQLFYWYEGLDHSA--ECTDYIKVGNKMGCRFPYLESSDYKDFYICVNS 216
DB 77 SSEPQ-ATNLTHRYRYKVSNNNTFQCSHYLFSKETTSQCQIQEDIQLYQTFVVL--Q 133
QY 217 SESQIRPSYFIFQONIVKMPDPYLSITVKNSEINLKNMKGPIPAKCFIYEIETP 276
DB 134 DPQKQRAVQKLNQNLVPRAPENLTLNLSSESOLELRWK--SRHIKERCLQLVQYR 191
QY 277 ED-GTTTWTTTTVENETQITRTS-NEQKLCFLVRKVNICYSDDGWSEWSEDCQWKGDI 334
DB 192 SNDRSRTWELIVNHEPRSLPSVDELKRYTFVRSYNPICGSSQOWSKWSQPVHWSHT 251
QY 335 WKETLVFF-----LIPFAPVSIFVLVITCLLY 362
DB 252 VEENPSLFALEAVLP--VGTMLIITLIFVY 281
RESULT 13
I45971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin receptor mRNA
A:Reference number: I45971; MUID:93246019
A:Accession: I45971
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C:Genetics:
A:Gene: PRLR
C:Superfamily: cytokine receptor homology
F:36-221/Domain: cytokine receptor homology <CRS>
Query Match 9.1%; Score 195; DB 2; Length 581;
Best Local Similarity 29.6%; Pred. No. 3.5e-07;
Matches 71; Conservative 31; Mismatches 88; Indels 50; Gaps 14;
QY 154 CSWKFGMGVHFDNNYQLFYWYEGLDHSAECTDYIKVGNKMGCRFPYLESSDYKDFYICV 213
DB 46 CWMEPCADGGLPTNTLTIVHKEGTLIHCEPDY-KTGGPN-SCYFSKKHTSIWKMYVIT 103
QY 214 N-----GSSESQPIRPSYFIFQONIVKMPDPYLSITVKNSEE----INLKNMMP-KGP 263
DB 104 NAINOMGISSDPL-----YVHVTVIPEPPANITLLEKHPEDRKPYLWIKWSPTMTD 158
QY 264 IPAKCFI--YEIEF-TEDGTTWVT--TTVENEIQITRTSNESQKLCFLVRKVNICYSD 318
DB 159 VKSGWFIQIYEIRLPERATDNEHTFLKQTLKIFNL-YPQKYLVLQIRCK-----PDH 212
QY 319 GIWSEWSDQCKW-----GDIWKEPLVFFLIPFAPVSIFVL-----VITCLL 360
DB 213 GYWSEWSPESIQIPNDPFVKDTSNW----IFVAILSAVICLIIMVMAVAKGYSMTCL 268
RESULT 14
A29884
prolactin receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000
C:Accession: A29884
R:Boutin, J.M.; Jolicœur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banvi
Cell 53, 69-77, 1988
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth
A:Reference number: A29884; MUID:88165059

Query Match 9.18; Score 194; DB 2; Length 412;
Best Local Similarity 27.7%; Pred. No. 2.7e-07;
Matches 75; Conservative 36; Mismatches 104; Indels 56; Gaps 13;

Qy 130 SPQGNRETKIQMDPCVYNWQYLVCSPKMGVHFEDTNLYQLFYWYEGLDHSAECTDYIKV 189
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 SPQKPEITH----KCRSPDKETFTFCWNPNPGDGLFPNYSLTYSKEGEKTYECPDY-KT 75

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:51:06 ; Search time 31.89 Seconds
(without alignments)
1344.449 Million cell updates/sec

Title: US-09-828-995B-61

Perfect score: 2132

Sequence: 1 MAFIHLDVGLYLLVCTAF.....LLKTIFHTKKEVSHQDTFC 386

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2132	100.0	386	22 AAU69135	Canine interleukin
2	2021	94.8	365	22 AAU69136	Canine interleukin
3	1775	83.3	318	22 AAU69137	Canine IL-13R extr
4	1775	83.3	561	22 AAU69138	Canine IL-13Ralpha
5	1775	83.3	561	22 AAU69141	Canine IL-13Ralpha
6	1775	83.3	563	22 AAU69140	Canine IL-13Ralpha
7	1775	83.3	565	22 AAU69139	Canine IL-13Ralpha
8	1503	70.5	380	18 AAU24972	Human interleukin-
9	1503	70.5	380	18 AAU35295	Human IL-13 bindin
10	1503	70.5	380	18 AAU36613	Human Zcytor2 cyto
11	1503	70.5	380	19 AAU41520	Human Zcytor2 cyto

12	1503	70.5	380	19 AAU41502	Human cytokine/pep
13	1503	70.5	380	19 AAU33603	Homo sapiens HR-1
14	1503	70.5	380	21 AAU95296	IL-13 binding chai
15	1503	70.5	380	22 AAG63812	Amino acid sequenc
16	1503	70.5	380	22 AAG72136	Human interleukin
17	1503	70.5	380	22 AAB29748	Human IL-13 recept
18	1480	69.4	380	18 AAU36614	Human Zcytor2 cyto
19	1473	69.1	372	18 AAU36616	Celebus macaque Zc
20	1417	66.5	255	22 AAU69134	Canine interleukin
21	1392.5	65.3	315	19 AAU56261	Mature interleukin
22	1392.5	65.3	359	19 AAU56260	Construct containi
23	1271.5	59.6	383	18 AAU35294	Murine IL-13 bindi
24	1271.5	59.6	383	21 AAU95295	IL-13 binding chai
25	1271.5	59.6	383	22 AAB72135	Murine interleukin
26	1271.5	59.6	383	22 AAB29747	Mouse IL-13 recept
27	791	37.1	145	22 AAU69133	Canine interleukin
28	345	16.2	426	18 AAU09821	Mouse interleukin-
29	329	15.4	426	18 AAU09822	Human interleukin-
30	320	15.0	157	19 AAU56252	Interleukin-13 bin
31	318.5	14.9	427	18 AAU24973	Human interleukin-
32	318.5	14.9	427	22 AAB19807	Human interleukin-
33	316.5	14.8	427	22 AAB19808	Human interleukin-
34	314	14.7	396	13 AAR22216	Sequence of human
35	313	14.7	421	13 AAR25064	Human IL-5 recepto
36	312.5	14.7	396	13 AAR22220	Sequence of secret
37	312.5	14.7	420	13 AAR22219	Sequence of secret
38	312	14.6	420	19 AAU82842	Human interleukin-
39	311	14.6	405	22 AAU69132	Canine interleukin
40	306	14.4	420	13 AAR22215	Sequence of human
41	304.5	14.3	793	21 AAU92208	IL-13/IL-4 dual tr
42	301	14.1	313	18 AAU21856	Protein used in pr
43	298	14.0	335	13 AAR25063	Soluble human IL-5
44	298	14.0	335	14 AAR33699	shIL-5R-alpha. Sy
45	298	14.0	1026	16 AAR70121	IL5-R-GBP 130 fusi

ALIGNMENTS

```

RESULT 1
AAU69135
ID AAU69135 standard; Protein; 386 AA.
XX
AC AAU69135;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine interleukin 13 receptor PcaIL-13Ralpha2 386.
XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX WPI: 2001-657172/75.
XX N-PSDB; AA55962.
XX
PT Novel isolated canine protein, preferably canine immunoglobulin G

```

protein or canine interleukin-13 receptor protein useful for regulating
immune response of an animal and for developing regulatory compounds -
XX
PS Claim 20; Page 176-177; 221pp; English.

The invention concerns an isolated canine protein, preferably canine Immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13R proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence represents a protein of the invention.

SQ Sequence 386 AA;

```
Query Match      100.0%; Score 2132; DB 22; Length 386;
Best Local Similarity 100.0%; Pred. No. 3e-198;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	MAFTHLDVGFLYTLVCTAFGSMLSNAEIKVNPQDPFEIVDPGYLYGYSULQWQPPFLFPDN	60
Db	1	mafhldvgflytlvctafgsmilsnaeikvnpqdpfeivdpgylygysulqwqpplfpgdn	60
Qy	61	FKECTIEVELKYRNIDSENWKTITIKNLHYKDGFDLNGKIEAKINTLLPAOCTNGSEVRS	120
Db	61	fkectievelkyrnidseawkttitknlhykdgfdlnkgleakintllpagctngsevrs	120
Qy	121	SWAETTYWTSPQGNRETKIQDMOCVYVNWQYLVCSSWKPGMVHPDTNYQLFWYEGLDHS	180
Db	121	swaettywtspqgnrekteiqdmocvvywnqylvcswkpgmvghdtnyqlfwyegldhs	180
Qy	181	AECTDYIKVGNKNGCRFPYLESSDYKDFYICVNGSSSQPIRPSYFIFQNTIVKMPPP	240
Db	181	aectdyikvngknmgcrfpylessdykdfyicvngssesqpirpsyfiqnlvkvkmppp	240
Qy	241	DYLSLTWKNSSEINLKNWMPKGPAPAKCFYIEIEFTEDGTTWVTTVNEIEQIRTSNES	300
Db	241	dylsltwknsseinelknwmpkgrpapakcfyieieftedgttwvttvneieqirtsnes	300
Qy	301	QKLCFLVRSKVNICYSDDGIWSEWSDEOCWKGDIWKETLVFFLPFAFVSVFLVITCLL	360
Db	301	qkclflvrskvnlycsddglwsewsdeqcwkgdiwketlvfflpfafvsvflvitlell	360
Qy	361	LYKORALLKTIFFHFKKEVFSHQDTFC	386
Db	361	lykorallktiffhckkevfhshqdtfc	386

RESULT	2
AAU69136	
ID	AAU69136 standard; Protein; 365 AA.
XX	
XX	AAU69136;
AC	
XX	
DT	29-JAN-2002 (first entry)
XX	
DE	Canine interleukin 13 receptor PcaIL-13Ralpha2 365.
XX	
KW	Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW	IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW	immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
KW	immune response.

XX	18-OCT-2001.
PD	
XX	
XX	09-APR-2001; 2001WO-US11498.
XX	
XX	
PR	07-APR-2000; 2000US-195659P.
PR	07-APR-2000; 2000US-195874P.
XX	
XX	(HESK-) HESKA CORP.
PA	
XX	
XX	McCall CA, Tang L;
XX	
XX	
DR	WPI; 2001-657172/75.
DR	N-PSDB; AAS59966.
XX	
PT	Novel isolated canine protein, preferably canine immunoglobulin G
PT	protein or canine interleukin-13 receptor protein useful for regulating
PT	immune response of an animal and for developing regulatory compounds -
XX	
PS	Claim 20; Page 181-183; 221pp; English.
XX	
CC	The invention concerns an isolated canine protein, preferably canine
CC	immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC	receptor protein, the nucleic acids encoding them, antibodies
CC	raised against them, fusion proteins between the IgG and IL-13R proteins
CC	and methods of isolating regulators of them. The regulators are useful
CC	for regulating an immune response in a canine. The proteins are useful
CC	to develop regulatory compounds including inhibitors and activators that,
CC	when administered to a canine in an effective manner, are capable of
CC	protecting canine from disease mediated by IL-13Ra1pha or IL-13. The
CC	regulators are useful for treating canine IgG (heavy and/or light chain)
CC	and/or canine IL-13R mediated responses. The molecules of the invention
CC	are useful to regulate the immune response of an animal (e.g. by gene
CC	therapy). The present sequence represents a protein of the invention.
XX	
XX	Sequence 365 AA;
SQ	

Query Match	94.8%;	Score	2021;	DB	22;	Length	365;
Best Local Similarity	100.0%;	Pred. No.	1.6e-187;				
Matches	365;	Conservative	0;	Mismatches	0;	Indels	0;
0;							
QY	22	SMLSNAEIKVNPQDFRIVDPGYGLYSLQWQPLRPDPNFKECTIEYELKYRNIDSENWK	81				
DB	1	smlsnaeikvnpqdfveivdpgyglyslqwdpplfpdnfkectieyelkyrnidsenwk	60				
QY	82	TIITKNLHYKGDGDLNKGIEAKINTLLPAQCTNGSEVRSSWAETTYWTSPOGNETRKIQD	141				
DB	61	tiitknlhykgdglngieakintllpaqctngsevrsswaettywtspgnretkicqd	120				
QY	142	MDCVYVNWQYLVCSWKPGMGVHPDNTVQLFVYWEGLDHSAECTDYTKVNGKNNMCCRPPYL	201				
DB	121	mdcvyvnwqylvcswkpgmgvhfdntnyqlfywgegldhsaectdytkvngknmgcrrpyl	180				
QY	202	ESSDYKDFYICVNGSSSQIRPSFYIFQLQNIKVMPDPDYLSTLVKNSSIEILKNWMPK	261				
DB	181	essdykdfyicvngssesqirpsfyifqlqniavkmpdpdylstlvknseeinlknwmpk	240				
QY	262	GPAPKCFYIEIEFTEDGTTWVITTVENETQIRTSNESOKLCFLVRSKYNIVCSDDGIIW	321				
DB	241	gpapakcfyieieftedgttwvittveneigqirtsnesqklcflvrskynivcsddgilw	300				
QY	322	SEWSDEOCWKGDJWKETPLVFPIPFAPVSIVLVITCLLYKORALLKTIFFHKKVEFSH	381				
DB	301	sewsdeocwkgdjwketylvlfpifpafvsiylvitcllykqralllktiffhckkevfish	360				
QY	382	QDFTC	386				
DB	361	qdtfc	365				

RESULT 3
AAU69137

AAU69137 standard; Protein: 318 AA.
AAU69137;
29-JAN-2002 (first entry)
Canine IL-13R extracellular domain PcaIL-13Ralpha2 318.
Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
immune response.
Canis familiaris.
WO200177332-A2.
18-OCT-2001.
09-APR-2001; 2001WO-US11498.
07-APR-2000; 2000US-195659P.
07-APR-2000; 2000US-195874P.
(HESK-) HESKA CORP.
McCall CA, Tang L;
WPI: 2001-657172/75.
N-PSDB; AAS59968.
Novel isolated canine protein, preferably canine immunoglobulin G
protein or canine interleukin-13 receptor protein useful for regulating
immune response of an animal and for developing regulatory compounds -
Claim 20; Page 185-187; 21pp; English.
The invention concerns an isolated canine protein, preferably canine
immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
receptor protein, the nucleic acids encoding them, antibodies
raised against them, fusion proteins between the IgG and IL-13R proteins
and methods of isolating regulators of them. The regulators are useful
for regulating an immune response in a canine. The proteins useful to
develop regulatory compounds including inhibitors and activators that,
when administered to a canine in an effective manner, are capable of
protecting canine from disease mediated by IL-13Ralpha or IL-13. The
regulators are useful for treating canine IgG (heavy and/or light chain)
and/or canine IL-13R mediated responses. The molecules of the invention
are useful to regulate the immune response of an animal (e.g. by gene
therapy). The present sequence represents a protein of the invention.
Sequence 318 AA;
Query Match 83.3%; Score 1775; DB 22; Length 318;
Best Local Similarity 100.0%; Pred. No. 1e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 SMLSNAEIKVNPQDFEIVDPGYLGYSLQWQPLFPDNFKECTIEYELKYNIDSENWK 81
DB 2 smlsnaeikvnpqdfelvdpgylgyslqwgplfpdnfkectieyelkynrdsenwk 61
QY 82 TIITKNLHYKDFDLNKIEAKINTLLPAQCTNGSEVSSWAETTYMTSPQGNRTKIQD 141
DB 62 tiitknlhykgdfdlngkieakintllpaqctngsevrsswaettywtspggnrtkikd 121
QY 142 MCVYVYNNQYLVCSWKKPGMGVHFDNTNQLFYWYEGSLDHSACTDYIKYNGKNMGCRFPYL 201
DB 122 mdcvynvnyqylvcswkpgmgvghfdntnqlfywyegldhsaectdyikvngknmgcrfpyl 181
QY 202 ESSDYKDFYICVNGSSSQIRPSYFFPOLQNIYKPMPPDYLSLTVKNSEINLKNWMPK 261
DB 182 essdykdfyicvngsssqirpsyffiqlnivkmpppdylsltvknseeinlknwmpk 241

QY 262 GPIPAKCFIYEIEFTEDGTTWVTTTENEIQITRTSNESQKLCFLVRSKVNIYCSDDGIW 321
DB 242 gpipakcfiyeieftedgttwvtttveneigqtrtsnesqklcflvrskvniycsddgiw 301
QY 322 SEWSDEQCWKGDIWKET 338
DB 302 sewsdeqcwkgdiwkwt 318
RESULT 4
AAU69138
ID AAU69138 standard; Protein: 561 AA.
XX AC
XX AAU69138;
XX 29-JAN-2002 (first entry)
XX DE
XX Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-3523 561.
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
XX IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
XX immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
XX immune response.
XX Canis familiaris.
XX OS
XX WO200177332-A2.
XX PN
XX 18-OCT-2001.
XX PD
XX 09-APR-2001; 2001WO-US11498.
XX PF
XX 07-APR-2000; 2000US-195659P.
XX PR 07-APR-2000; 2000US-195874P.
XX DR (HESK-) HESKA CORP.
XX FA
XX McCall CA, Tang L;
XX PI
XX WPI: 2001-657172/75.
XX DR N-PSDB; AAS59970.
XX PS
XX Novel isolated canine protein, preferably canine immunoglobulin G
XX protein or canine interleukin-13 receptor protein useful for regulating
XX immune response of an animal and for developing regulatory compounds -
XX Claim 46; Page 191-193; 21pp; English.
XX The invention concerns an isolated canine protein, preferably canine
XX immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
XX receptor protein, the nucleic acids encoding them, antibodies
XX raised against them, fusion proteins between the IgG and IL-13R proteins
XX and methods of isolating regulators of them. The regulators are useful
XX for regulating an immune response in a canine. The proteins useful to
XX develop regulatory compounds including inhibitors and activators that,
XX when administered to a canine in an effective manner, are capable of
XX protecting canine from disease mediated by IL-13Ralpha or IL-13. The
XX regulators are useful for treating canine IgG (heavy and/or light chain)
XX and/or canine IL-13R mediated responses. The molecules of the invention
XX are useful to regulate the immune response of an animal (e.g. by gene
XX therapy). The present sequence represents a protein of the invention.
XX Sequence 561 AA;
Query Match 83.3%; Score 1775; DB 22; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.3e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 SMLSNAEIKVNPQDFEIVDPGYLGYSLQWQPLFPDNFKECTIEYELKYNIDSENWK 81
DB 2 smlsnaeikvnpqdfelvdpgylgyslqwgplfpdnfkectieyelkynrdsenwk 61

QY 82 TITKLNHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRSSWAETTYWTSPQGNRETQIOD 141
 |||||
 DB 62 ttiitknlhykdgfdlnkgleakintllpaqctngsevrsswaettywtspqgnrekiqd 121
 |||||
 QY 142 MDCVYNNWOYLVCSSWKPGMGVHFDNTNYQLFYWYEGLDHSAECTDYIKVNGKNMGCRFPYL 201
 |||||
 DB 122 mdcvyywnwqylvcswkpgmgvghfdntnyqlfywyegldhsaectdyikvngknmgcrfpyl 181
 |||||
 QY 202 ESSDYKDFYICVNGSSESQPIRPSYFIFOLQNTVKNPMPDPDYLSTVKNSEENLKNWMPK 261
 |||||
 DB 182 essdykdfyicvngsseqprrpsyfifqlqnlvknmpdpdyislvtknseeinlknwmpk 241
 |||||
 QY 262 GPIPAKCFIYEIEFTEDGTTWTTTVEINEIQITRTSNESQKLCFLVRSKNVNYCSDGDIW 321
 |||||
 DB 242 gpipakcfiyeieftedgttwtvtvneiqitrtstnesqkicflvrskvniycsddgiw 301
 |||||
 QY 322 SEWSDQCKWGDWIKET 338
 |||||
 DB 302 sewsdeqckwgdwiket 318
 |||||
 RESULT 5
 AAU69141
 ID AAU69141 standard; Protein; 561 AA.
 AC AAU69141;
 DT 29-JAN-2002 (first entry)
 XX Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-B9 561.
 DE Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
 KW immune response.
 XX Canis familiaris.
 OS
 PN WO200177332-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 09-APR-2001; 2001WO-US11498.
 XX
 PR 07-APR-2000; 2000US-195659P.
 PR 07-APR-2000; 2000US-195874P.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI McCall CA, Tang L;
 XX
 DR WPI; 2001-657172/75.
 DR N-PSDB; AAS59976.
 XX
 PS Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -
 XX
 PS Claim 46; Page 210-212; 221pp; English.
 XX
 CC The invention concerns an isolated canine protein, preferably canine
 CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
 CC receptor protein, the nucleic acids encoding them, antibodies
 CC raised against them, fusion proteins between the IgG and IL-13R proteins
 CC and methods of isolating regulators of them. The regulators are useful
 CC for regulating an immune response in a canine. The proteins useful to
 CC develop regulatory compounds including inhibitors and activators that,
 CC when administered to a canine in an effective manner, are capable of
 CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
 CC regulators are useful for treating canine IgG (heavy and/or light chain)
 CC and/or canine IL-13R mediated responses. The molecules of the invention
 CC are useful to regulate the immune response of an animal (e.g. by gene

CC therapy). The present sequence represents a protein of the invention.
 XX
 SQ Sequence 561 AA;
 Query Match 83.3%; Score 1775; DB 22; Length 561;
 Best Local Similarity 100.0%; Pred. No. 2.3e-163;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 SMLSNAEIKVNPQDPEIVDPGVLGVLQWQPPPLPPDNFKECTIYELKYRNIDSENWK 81
 |||||
 DB 2 smlsnaeikvnpqdfelvdpgylglslqwdppilfpdnfkectieyelkyrnidsewnk 61
 |||||
 QY 82 TITKLNHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRSSWAETTYWTSPQGNRETQIOD 141
 |||||
 DB 62 ttiitknlhykdgfdlnkgleakintllpaqctngsevrsswaettywtspqgnrekiqd 121
 |||||
 QY 142 MDCVYNNWOYLVCSSWKPGMGVHFDNTNYQLFYWYEGLDHSAECTDYIKVNGKNMGCRFPYL 201
 |||||
 DB 122 mdcvyywnwqylvcswkpgmgvghfdntnyqlfywyegldhsaectdyikvngknmgcrfpyl 181
 |||||
 QY 202 ESSDYKDFYICVNGSSESQPIRPSYFIFOLQNTVKNPMPDPDYLSTVKNSEENLKNWMPK 261
 |||||
 DB 182 essdykdfyicvngsseqprrpsyfifqlqnlvknmpdpdyislvtknseeinlknwmpk 241
 |||||
 QY 262 GPIPAKCFIYEIEFTEDGTTWTTTVEINEIQITRTSNESQKLCFLVRSKNVNYCSDGDIW 321
 |||||
 DB 242 gpipakcfiyeieftedgttwtvtvneiqitrtstnesqkicflvrskvniycsddgiw 301
 |||||
 QY 322 SEWSDQCKWGDWIKET 338
 |||||
 DB 302 sewsdeqckwgdwiket 318
 |||||
 RESULT 6
 AAU69140
 ID AAU69140 standard; Protein; 563 AA.
 XX
 AC AAU69140;
 DT 29-JAN-2002 (first entry)
 XX
 DE Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-B9 563.
 KW Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
 KW immune response.
 XX Canis familiaris.
 OS
 PN WO200177332-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 09-APR-2001; 2001WO-US11498.
 XX
 PR 07-APR-2000; 2000US-195659P.
 PR 07-APR-2000; 2000US-195874P.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI McCall CA, Tang L;
 XX
 DR WPI; 2001-657172/75.
 DR N-PSDB; AAS59974.
 XX
 PS Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -
 XX
 PS Claim 46; Page 203-206; 221pp; English.
 XX

CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins are useful
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence represents a protein of the invention.
XX
SQ .Sequence 563 AA;

Query Match 83.3%; Score 1775; DB 22; Length 563;
Best Local Similarity 100.0%; Pred. No. 2.3e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 SMLSNAETKVPDPDFEIVDPGYLGYSLOWQPPPLFPDNFKECTIEYELKYRNIDSENWK 81
Db 2 smlsnaekvnpdpqdfvdpgylyslqwpplfpdnfkectieyelkynidsenwk 61
Qy 82 TIITKNLHYKGFDLNKGIEAKINTLLPAQCTNGSEVRSSWAETTYTSPQGNRETKIOD 141
Db 62 tiitknlhykgdflnkgieakintltpaqtngsevrsswaettytspqgnretkiqd 121
Qy 142 MDCVYNNQYLVCSWKPGMGVHFDNTYOLFVWYEGLDHSAECTDYIKVNGKNMGRFPYL 201
Db 122 mdcvynwqyivcswkpgmgvhfdntnyqlfywyegldhsaectdyikvngknmgerfpyl 181
Qy 202 ESSDYKDFYICVNGSSESQPIRPSYFIFQLQNIKVPMPDYLSTLVKNSEELNKNMMPK 261
Db 182 essdykdfyicvngssesqpirpsyfflqlqnivkmpdpdylsltkvnselnlknmmpk 241
Qy 262 GPIPAKCFIYEIEFTEDGTTWVTTTENEIQITRTSNESQKLCFLVRSKVNIYCSDDGIW 321
Db 242 gpipakcfiyeieftedgttwtvtteneiqitrtsneskqlcflvrskvniycsddgiw 301
Qy 322 SEWSDQCWKGDWIKET 338
Db 302 sewsdeqcwkgdwiket 318

RESULT 7
AAU69139 standard; protein; 565 AA.
XX AAU69139;
AC AAU69139;
XX
DT 29-JAN-2002 (first entry)
XX
XX Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-4325 565.
DE
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
XX WO200177332-A2.
XX
XX 18-OCT-2001.
PD
XX 09-APR-2001; 2001WO-US11498.
PF
XX 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
XX (HESK-) HESKA CORP.

XX McCall CA, Tang L;
PI
XX
XX WPI: 2001-657172/75.
DR N-PSDB; AAS59972.
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX Claim 46; Page 197-199; 221pp; English.
PS
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins are useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence represents a protein of the invention.
XX
SQ Sequence 565 AA;

Query Match 83.3%; Score 1775; DB 22; Length 565;
Best Local Similarity 100.0%; Pred. No. 2.3e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 SMLSNAETKVPDPDFEIVDPGYLGYSLOWQPPPLFPDNFKECTIEYELKYRNIDSENWK 81
Db 2 smlsnaekvnpdpqdfvdpgylyslqwpplfpdnfkectieyelkynidsenwk 61
Qy 82 TIITKNLHYKGFDLNKGIEAKINTLLPAQCTNGSEVRSSWAETTYTSPQGNRETKIOD 141
Db 62 tiitknlhykgdflnkgieakintltpaqtngsevrsswaettytspqgnretkiqd 121
Qy 142 MDCVYNNQYLVCSWKPGMGVHFDNTYOLFVWYEGLDHSAECTDYIKVNGKNMGRFPYL 201
Db 122 mdcvynwqyivcswkpgmgvhfdntnyqlfywyegldhsaectdyikvngknmgerfpyl 181
Qy 202 ESSDYKDFYICVNGSSESQPIRPSYFIFQLQNIKVPMPDYLSTLVKNSEELNKNMMPK 261
Db 182 essdykdfyicvngssesqpirpsyfflqlqnivkmpdpdylsltkvnselnlknmmpk 241
Qy 262 GPIPAKCFIYEIEFTEDGTTWVTTTENEIQITRTSNESQKLCFLVRSKVNIYCSDDGIW 321
Db 242 gpipakcfiyeieftedgttwtvtteneiqitrtsneskqlcflvrskvniycsddgiw 301
Qy 322 SEWSDQCWKGDWIKET 338
Db 302 sewsdeqcwkgdwiket 318

RESULT 8
AAW24972 standard; protein; 380 AA.
ID AAW24972
XX
XX AAW24972;
AC
XX
XX 22-JUN-1998 (first entry)
DT
XX Human interleukin-13 beta receptor.
DE
XX Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
KW
XX Homo sapiens.
OS
XX WO9720926-A1.
PN

SQ Sequence 380 AA;
 Query Match 70.5%; Score 1503; DB 18; Length 380;
 Best Local Similarity 72.9%; Pred. No. 3.3e-137;
 Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;
 QY 1 MAFIHLVDGFLYTLVCTAFG-SMLSNAEIKVNPQDFEIVDPGVLGYSLQWQPPLPDD 59
 Db 1 mafvclgaicgyltflstfctsssdteikvnpqdfvdpvglylylqwgpplsld 60
 QY 60 NRECECTIEVELKYRNIDSENWKTITKLNHYKDGFDLNGKIEAKINTLLPAQCTNGSEVR 119
 Db 61 hfrectvevelkyrnigsetwtiitknlhykdgfdlnkgleakhtllpwqctngsevg 120
 QY 120 SSWAETTYTSPQGNRETKIQDMDCVYVYNNQYLVCWSKPGMGVHFDNTNYQLFYWYEGLDH 179
 Db 121 sswaettywispagipetkvqmdcvyynqylyllcswkpgigvllidtnynlfywyegldh 180
 QY 180 SACTDYIKVNGKNMCRFPYLESSDYKDFYICVNGSSESQPIRPSYFIFQLQNIWKPM 239
 Db 181 alqcvdyikadgnicrpfyleasdykdfycvngssenkpirssyftfqlqnvkplp 240
 QY 240 PDVLSLTVKNSEINLKNWPKGPIPAKCFIYEIEFTEDGTWVTWTTVENEIOIIRTSNE 299
 Db 241 pvylltfressceiklkwslpigrparcfyieireddttlvtatvenetytkttne 300
 QY 300 SOKLCFLVRSKVNIYCSDDGINSWSEDCQWKG-DIWKETLVFFLIPPAFVSIFVLVITC 358
 Db 301 trqlcfvrskvniycsdgigwsewskqcgwedlskktllrfwlpfgfllilvifvtg 360
 QY 359 LLLYKQKRALKTI 371
 Db 361 llrrkntypkmi 373
 RESULT 11
 AAW41520
 ID AAW41520 standard; Protein; 380 AA.
 XX
 AC AAW41520;
 XX
 DT 22-JUN-1998 (first entry)
 XX Human HR-1 receptor.
 DE
 XX HR-1 receptor; human; cytokine; infection; asthma; allergy;
 KW haematopoietic disorder; tumour; therapy; diagnosis.
 DR N-PSDB; AAT96782.
 New nucleic acid encoding testis-specific cytokine receptor - useful for identification of ligands or antagonists, potentially for use as male contraceptives or for infertility treatment
 Claim 2: Page 47-48; 79pp; English.
 This sequence represents a novel ligand-binding receptor, *zcytor2*, which shares homology with cytokine receptors and was isolated from human placental polyA+ RNA. The resulting polypeptide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to treat infertility. Antagonists of this receptor may be used to characterise ligand-receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulating levels of ligand and also to isolate and purify ligands. Antibodies can be used to assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor, and therapeutically as antagonist.
 Query Match 70.5%; Score 1503; DB 18; Length 380;
 Best Local Similarity 72.9%; Pred. No. 3.3e-137;
 Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;
 QY 1 MAFIHLVDGFLYTLVCTAFG-SMLSNAEIKVNPQDFEIVDPGVLGYSLQWQPPLPDD 59
 Db 1 mafvclgaicgyltflstfctsssdteikvnpqdfvdpvglylylqwgpplsld 60
 QY 60 NRECECTIEVELKYRNIDSENWKTITKLNHYKDGFDLNGKIEAKINTLLPAQCTNGSEVR 119
 Db 61 hfrectvevelkyrnigsetwtiitknlhykdgfdlnkgleakhtllpwqctngsevg 120
 QY 120 SSWAETTYTSPQGNRETKIQDMDCVYVYNNQYLVCWSKPGMGVHFDNTNYQLFYWYEGLDH 179
 Db 121 sswaettywispagipetkvqmdcvyynqylyllcswkpgigvllidtnynlfywyegldh 180
 QY 180 SACTDYIKVNGKNMCRFPYLESSDYKDFYICVNGSSESQPIRPSYFIFQLQNIWKPM 239
 Db 181 alqcvdyikadgnicrpfyleasdykdfycvngssenkpirssyftfqlqnvkplp 240
 QY 240 PDVLSLTVKNSEINLKNWPKGPIPAKCFIYEIEFTEDGTWVTWTTVENEIOIIRTSNE 299
 Db 241 pvylltfressceiklkwslpigrparcfyieireddttlvtatvenetytkttne 300
 QY 300 SOKLCFLVRSKVNIYCSDDGINSWSEDCQWKG-DIWKETLVFFLIPPAFVSIFVLVITC 358
 Db 301 trqlcfvrskvniycsdgigwsewskqcgwedlskktllrfwlpfgfllilvifvtg 360
 QY 359 LLLYKQKRALKTI 371
 Db 361 llrrkntypkmi 373
 RESULT 11
 AAW41520
 ID AAW41520 standard; Protein; 380 AA.
 XX
 AC AAW41520;
 XX
 DT 22-JUN-1998 (first entry)
 XX Human HR-1 receptor.
 DE
 XX HR-1 receptor; human; cytokine; infection; asthma; allergy;
 KW haematopoietic disorder; tumour; therapy; diagnosis.
 DR WPI; 1997-470820/43.

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XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT Protein /label= Sig_peptide
XX FT 22..380
XX FT /label= Mat_protein
XX PN WO9747741-A1.
XX PD 18-DEC-1997.
XX PF 12-JUN-1996; 96WO-US10262.
XX PR 12-JUN-1996; 96WO-US10262.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Appelbaum ER, Hu J;
XX KW WPI: 1998-052308/05.
XX DR N-PSDB; AAV04131.
XX OS Nucleic acid sequence encoding human cytokine peptide hormone
XX PT receptor - useful to treat, prevent or diagnose, e.g. lowered
XX PT resistance to infection, asthma, allergy or haematopoietic disease
XX PS Claim 13; Page 62-64; 76pp; English.
XX CC This protein comprises a novel human cytokine/peptide hormone
XX CC receptor, designated the HR-1 receptor, that shows 27% identity
XX CC and 52% similarity to the interleukin-5 receptor. Its amino acid
XX CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a
XX CC human testis library. Recombinant HR-1 receptor can be expressed
XX CC in claimed host cells, and used in a claimed method for identifying
XX CC compounds which bind to, and activate or inhibit, it. HR-1
XX CC receptor activators and agonists can be used to treat, prevent or
XX CC diagnose predisposition to lowered resistance to infection, asthma,
XX CC allergic or haematopoietic disorders, e.g. where induced by AIDS,
XX CC aplastic anaemia, neutropaenia or cytotoxic treatments for cancer.
XX CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
XX CC be used to treat conditions associated with HR-1 receptor
XX CC overexpression. The antibodies can also be used to determine HR-1
XX CC receptor levels, since overexpression may be diagnostic of tumours.
XX CC Sequence 380 AA;
XX QY 1 MAFIHLDVGLYTLVCTAFG-70.5%; Score 1503; DB 19; Length 380;
XX DB 1 mafvclalgcltyflsttfgctssdssteikvnpqpdfeivdpqylgylqwpplslid 59
XX QY 60 NEKECTIEVELKYRIDSNNWTKITKLNHYKDGFDLNGKIEAKINTLLPAQCTNGSEVR 119
XX DB 61 hfrectvvelkyrignsetwtitknlnhykdgdlnkgieakhtlplwqctngsevg 120
XX QY 120 SSWAETTYTSPQGNRETKIQDMDCVYVYNNQYLVCWSKPGMGVHFDNTNYQLFYWYEGLDH 179
XX DB 121 sswaettyvispgqipetkvqmdcvyynwqylleswkpgigvldntnlyfwyegldh 180
XX QY 180 SAECTDYIKVNGKMGCRPPYLESSDYKDFYICVNGSSSQIRPSYFTFQLQNIYKMP 239
XX DB 181 alqcvdylkadgngicrfpyleasdykdfycvngsssenkplrssyftfqlqniwkplp 240
XX QY 240 PLYLSITVKNSEINLKNWPKGPIPAKCFIYEIEFTEDGTTWTTVTVNEIQITTSNE 299
XX DB 241 pylvltftrssceiklkwsqipgiparcfdyeleireddttlvtatvenetytiktne 300
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QY 300 SOKLCFLVRSKVNIYCSDDGIWSEMSDEOCWKG-DIWKETLVFELIPFAFVIFVLVITC 358
DB 301 trqlcfvvrskvniycsddgiwsewskqcgwedlskktllrfwlpfgfllilvifvvg 360
QY 359 LLLYKORALLKTI 371
DB 361 lllrkpntypkmi 373
RESULT 12
AAW41502
ID AAW41502 standard; Protein; 380 AA.
XX AC AAW41502;
XX DT 08-JUN-1998 (first entry)
XX DE Human cytokine/peptide receptor, HR-1 receptor.
XX KW HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
XX KW infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
XX KW neutropaenia; therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT Protein /label= Sig_peptide
XX FT 22..380
XX FT /label= Mat_protein
XX FT /note= "Claim 14"
XX EP812913-A2.
XX PD 17-DEC-1997.
XX PF 04-JUN-1997; 97EP-0303815.
XX PR 12-JUN-1996; 96US-0017843.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Appelbaum ER, Hu J;
XX DR WPI: 1998-034974/04.
XX DR N-PSDB; AAV04075.
XX PT Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
XX PT increase resistance to infections in individuals with trauma and/or
XX PT burns
XX PS Claim 13; Page 27-28; 34pp; English.
XX CC This protein comprises a novel human cytokine/peptide hormone
XX CC receptor, designated HR-1 receptor. The amino acid sequence
XX CC was deduced from a cDNA clone (see AAV04075) isolated from a human
XX CC testis cDNA library. It shows 27% amino acid identity and 52%
XX CC similarity with the human interleukin-5 receptor. Also claimed are
XX CC polynucleotides encoding HR-1 receptor, vector and host cells, an
XX CC agonist to the polypeptide, antibody against the polypeptide, an
XX CC antagonist that inhibits the activity of the polypeptide, a process
XX CC for diagnosing a disease, or a susceptibility to disease, related
XX CC to expression of HR-1 receptor, and a method for identifying
XX CC compounds that activate or inhibit the HR-1 receptor. HR-1
XX CC receptor protein and polynucleotides can be used for research,
XX CC biological, diagnosis and (gene) therapy applications, e.g. to
XX CC increase resistance to infections in individuals with trauma and/or
XX CC burns, and to prevent, ameliorate, treat, diagnose and/or determine
XX CC predisposition to asthma, allergic disorders or disorders of
XX CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or
XX CC cyclic neutropaenia or as a consequence of cytotoxic therapy of
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PI Appelbaum ER, Hu J;

Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
cytokine receptor; haematopoietin receptor; atopy; allergy; asthma
immune complex disease; lupus; nephritis; thyroiditis;
Grave's disease; inflammatory; infection; therapy; antiallergic;
antiinflammatory; antiasthmatic; vaccine.

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